Validation: Understanding CheckCIF for small molecules

Larry R. Falvello
Universidad de Zaragoza – CSIC
Departamento de Química Inorgánica e ICMA
Pedro Cerbuna 12
50009 Zaragoza
falvello@unizar.es

AICS2019 - Crystallographic Information Fiesta
1 September, 2019

www.chemcrystal.org

Summary

Validation: Understanding CheckCIF for small molecules

A brief description of the historical background of, and motivation for, small-molecule structure validation is used to introduce the logical structure of CheckCIF and the categories of tests that it conducts. The corresponding categories of alerts are presented, and examples are given of selected alerts and appropriate actions in response to those alerts. Emphasis is placed throughout on the main issues addressed by CheckCIF:

- - Completeness and self-consistency of the data provided in the CIF;
- - Detection of errors or important deficiencies in the structure analysis;
- - Estimation of the quality of the structure analysis.

The presentation concludes with a suggested strategy for practical and efficient use of structure validation in a small-molecule crystal structure analysis.

Historical Background

Some information on early thoughts is given here:

Commission on Crystallographic Teaching

International Union of Crystallography

Newsletter No. 2, November 2007

https://www.iucr.org/resources/commissions/crystallographic-teaching/newsletters/2

The History of the ORTEP of the Year ("OOTY") Award

Richard L. Harlow

'I found that the most common point of interest (among chemists at Dupont) was around the issue of how a chemist could tell a reliable crystal structure from an incorrect one,….'

Troublesome Crystal Structures: Prevention, Detection, and Resolution.

Richard L. Harlow. J. Res. Natl. Inst. Stand. Technol. 101, 327-339 (1996)

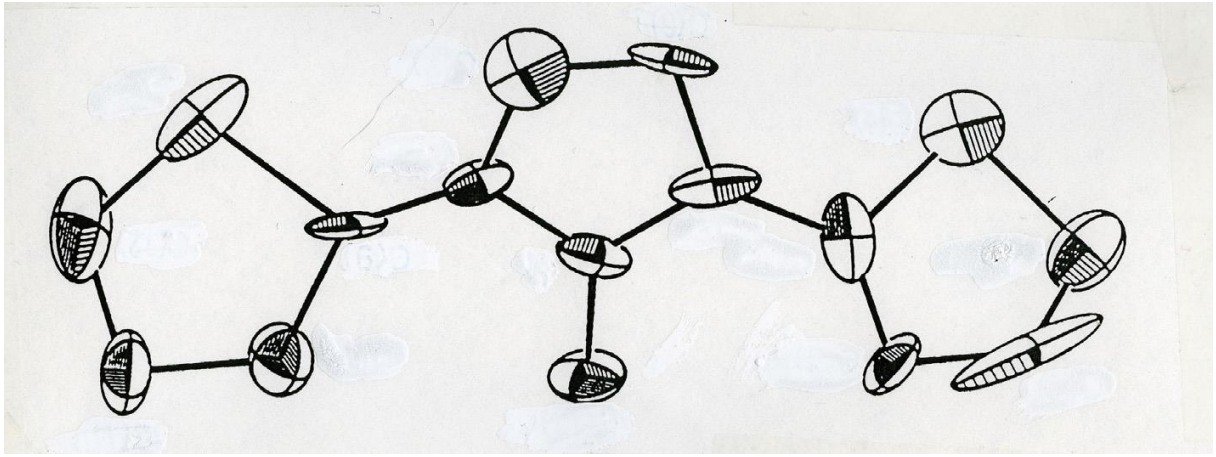
Crystallographic Data Validation – Ten Years On

Anthony Linden

'The validation of crystal structures became a formal procedure in late 1997 with the introduction of the *checkCIF* software by the *IUCr* journals. This was an initiative of Syd Hall who was Section Editor of *Acta Crystallographica Section C* at the time. Together with Mike Hoyland of the *IUCr* Chester office and Ton Spek from Utrecht University, author of *PLATON*, the Chester *checkCIF* suite was developed and augmented with additional tests incorporated in *PLATON*.'

Historical Background

The ORTEP of the Year Award was first inspired by the structure analysis represented in the drawing. An important feature of this drawing, which indicates that something is likely to be wrong, is the diversity of displacement parameters.



Motivation for Small-Molecule Structure Validation

To ease the load on the human operator. Structure determination has become much more rapid than it was a half- or quarter-century ago. The number of structure analyses that can be done in a given time by one operator is usually more than one person can validate.

To improve the efficiency of the crystal-structure-determination process as a whole. If the laborious aspects of results-checking can be automated, the operator will be free to concentrate on those parts of the procedure that need human intervention – such as interpreting the chemical implications of the results.

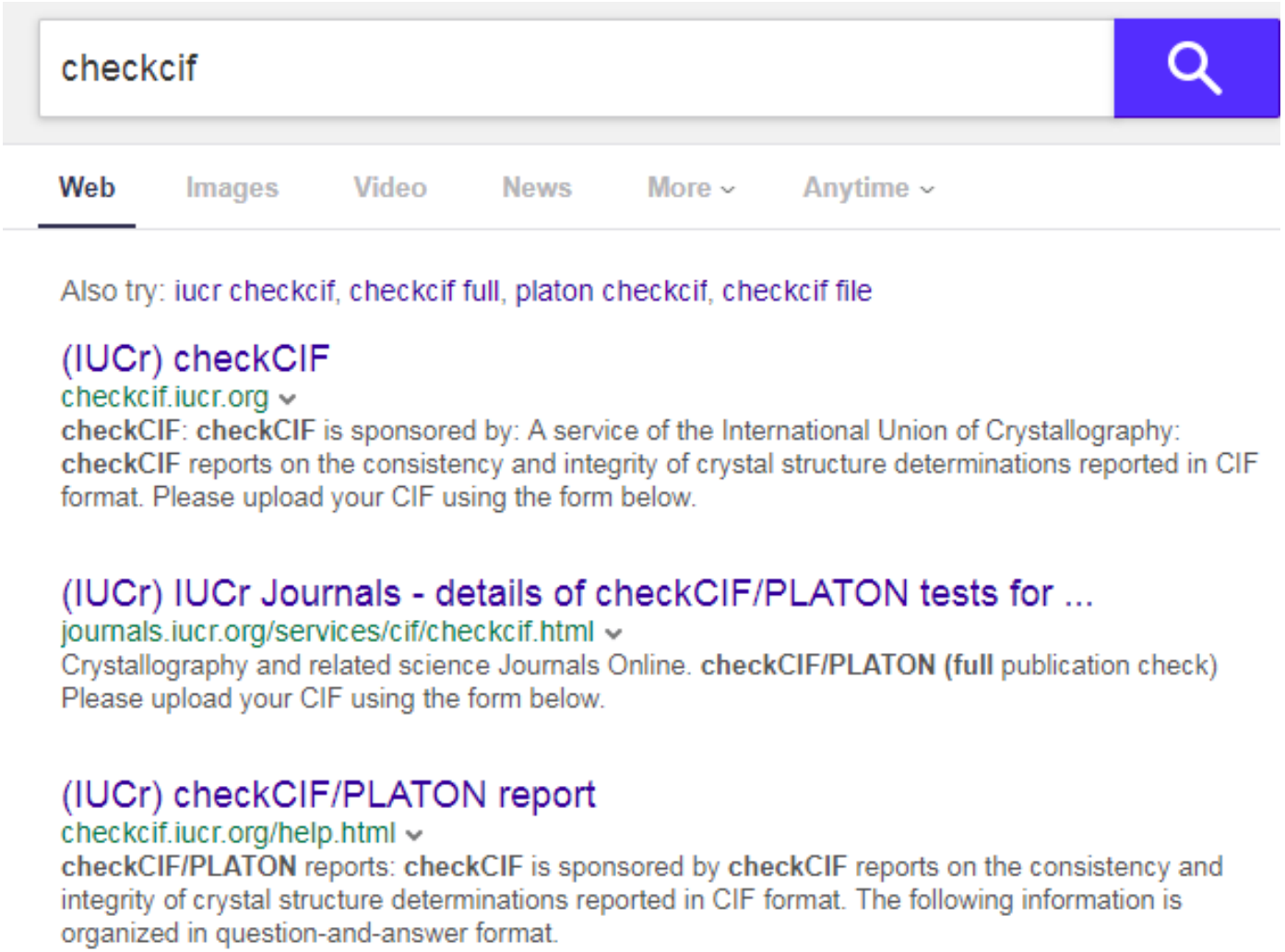
To assist those users who have not had detailed crystallographic training. Advances in hardware and software have brought accurate crystal structure determination to within reach of a large and growing number of scientists whose expertise lies in other areas, such as synthetic chemistry. Structure validation can assist in identifying potential problems in the results of a structure analysis, in some cases even when the primary quality indicators (R-factors) do not signal a problem.

Computerized structure validation can be viewed as a tool that **partially** automates an important part of crystal structure analysis, namely quality control.

Note that structure validation can be useful at any stage of a structure analysis.

Running CheckCIF

You can get to the CheckCIF web page through your favorite search engine.



Running CheckCIF

What it is based on

Small-molecule structure validation is based conceptually on three questions:

- Is the structure analysis correct?
- What is the quality of the structure analysis?
- Is the information provided complete and self-consistent?

The quality of a crystal structure analysis, reflected in the answers to the first two questions, can be classified within one of four groups:

- "**Class I:**" High-quality analyses from near-ideal crystals with diffraction measured under optimal experimental conditions such as low temperature and high resolution.
- "**Class II:**" "Good" structure determinations obtained under routine conditions but not the highest attainable quality. This could include room-temperature studies or analyses from large, irregularly shaped highly absorbing samples, or unusually rapid data collection.
- "**Class III:**" These are "poor quality" analyses which are nevertheless correct for the purposes of the study. The quality issues could arise from incomplete data, bad crystal quality, or a modelling problem such as severe disorder.
- "**Class IV:**" These are analyses that are incorrect in a manner relevant to the conclusions drawn from them. A bad element assignment, or an incorrect hybridization for a carbon atom (reflected in the number of hydrogen atoms bonded to it) may originate such results.

What it is based on

Small-molecule structure validation is based conceptually on three questions:

- Is the structure analysis correct?
- What is the quality of the structure analysis?
- Is the information provided complete and self-consistent?

(continued from previous slide)

For the third question – about complete and self-consistent data – a checklist is used to perform tests for this.

For the first two questions – is the analysis correct and what is its quality? – it is not possible to invoke a set of rigorous, objective , computer-ready tests for classifying a structure analysis into one of the four classes.

Instead, for CheckCIF/PLATON a set of tests has been devised which produce their corresponding alerts when the software detects a condition that may need user intervention. In this sense, CheckCIF/PLATON is informative and the user is responsible for evaluating the structure analysis in the light of the alerts and for taking any corrective action necessary. In some cases all that is needed is further explanation in the CIF or journal article.

CheckCIF/PLATON tests -- overview

Note. Small molecule structure validation, as presently implemented, is closely tied to the use of CIF for reporting the results of structure analyses. CIF as a standard for communicating the results of structure determinations, has been a strong enabling factor in the development of CheckCIF and in its facile implementation and use throughout the scientific community.

In the absence of clear, objective, programmable criteria for classifying structure analyses into the four quality categories given earlier, validation in CheckCIF/PLATON conducts a large number of tests, which can produce ALERTS that fall into one of four classes, depending on the potential severity of the condition that causes the alert. The validation criteria have evolved with time, and are in general based on knowledge, experience and current best practices.

Now that most CIF produced by structure refinement programs also contain the reflection data, CheckCIF/PLATON can perform very useful tests using the data, such as a test for twinning.

CheckCIF/PLATON tests -- overview

There are four general types of validation test, and there are alerts of four levels of possible severity.

Classes of validation test [verbatim, from Spek (2009)]:

1. Missing or inconsistent data.
2. Indicators that the structure model may be wrong or deficient.
3. Indicators that the quality of the results of the study may be low.
4. Cosmetic improvements, queries and suggestions.

Levels of alert (verbatim, from the code):

ALERT_Level_A = Could Indicate a Serious Problem - Consider Carefully.
ALERT_Level_B = Might Indicate a Potentially Serious Problem.
ALERT_Level_C = Check to Ensure it is OK and not Because of an Oversight.
ALERT_Level_G = General Info. Check that it is not Something Unexpected.

CheckCIF/PLATON tests -- overview

Summarizing: We cannot (yet) program a good, objective set of criteria for classifying structures into the four quality classes that we have defined. But we do have a large number of tests that can reveal localized problems with the results as well as more subtle defects that may be identified through combinations of alerts.

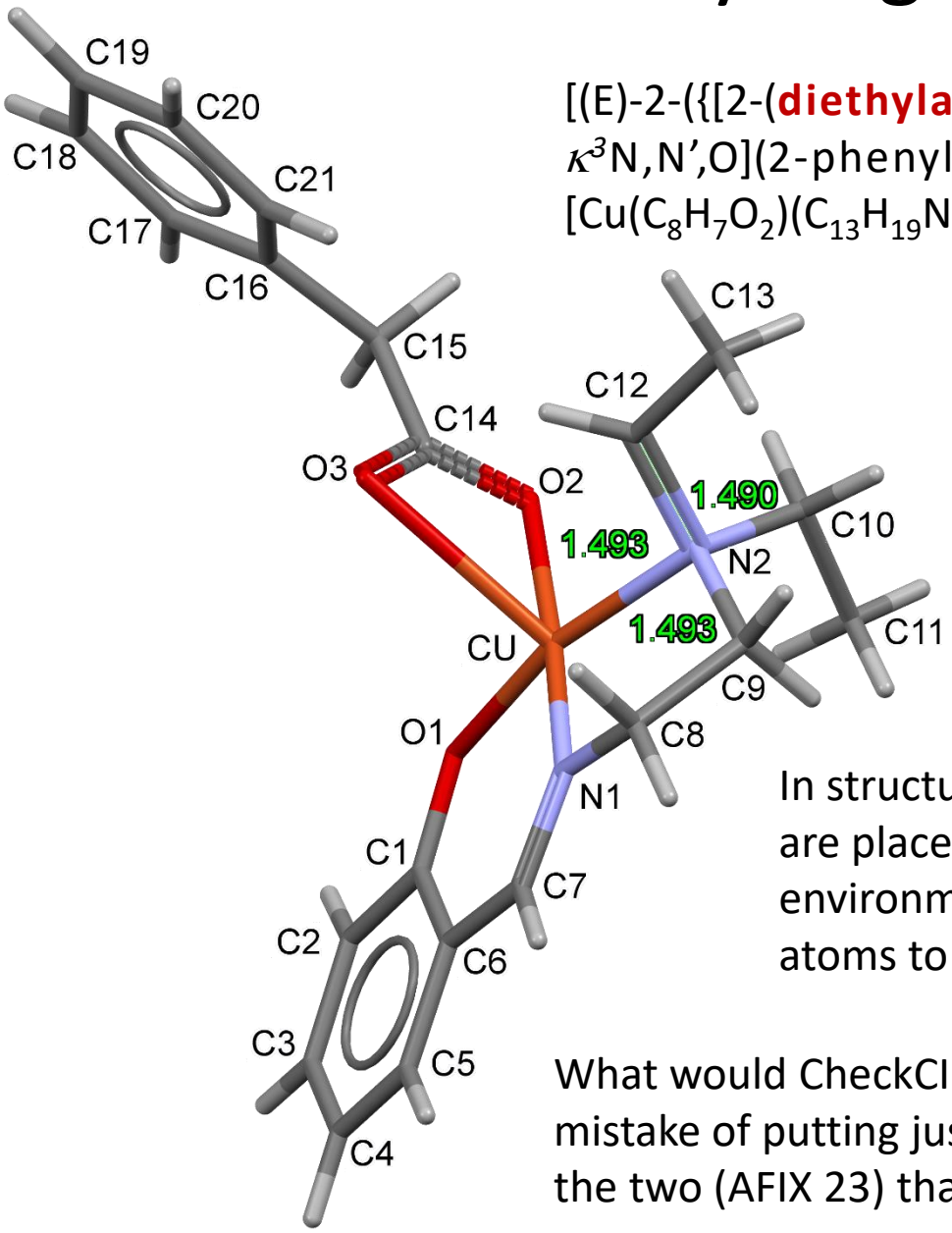
In addition, a computerized checklist is used to test whether the reported results are complete and self-consistent.

Levels of alert (verbatim, from the code):
ALERT_Level_A = Could Indicate a Serious Problem - Consider Carefully.
ALERT_Level_B = Might Indicate a Potentially Serious Problem.
ALERT_Level_C = Check to Ensure it is OK and not Because of an Oversight.
ALERT_Level_G = General Info. Check that it is not Something Unexpected.

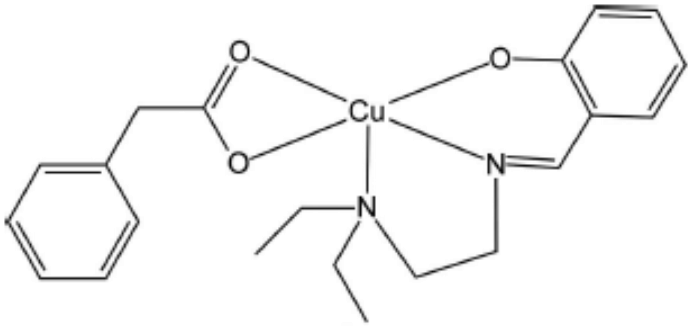
Today's CheckCIF Tests

- Tests are identified with three-digit numbers
_0xx - general
_1xx - cell/symmetry
_2xx - adp-related
_3xx - intra geometry
_4xx - inter geometry
_5xx - coordination geometry
_6xx - void tests & varia
_7xx - varia
_8xx - (Fatal) Software Errors/Problems
_9xx - Reflection data issues

A hydrogen-atom issue



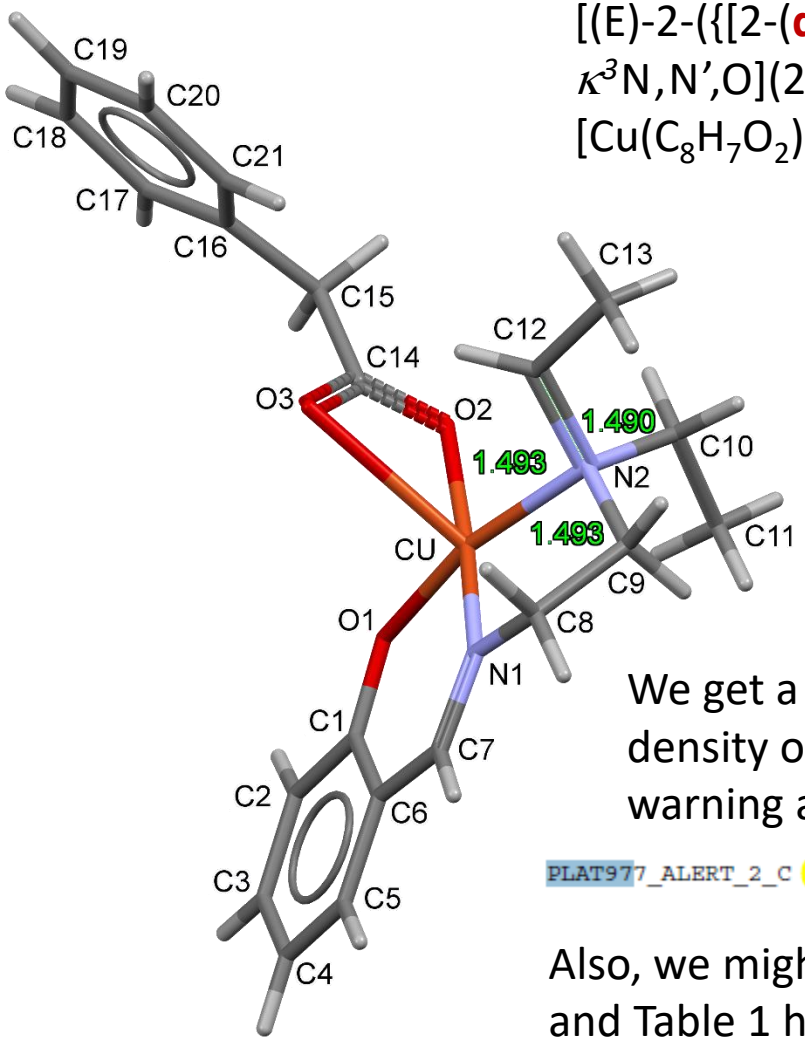
[(E)-2-({[2-(**diethylamino**)ethyl]imino}methyl)phenolato-κ^3N,N',O](2-phenylacetato-κ^2O,O')copper(II), $[Cu(C_8H_7O_2)(C_{13}H_{19}N_2O)]$, **2**



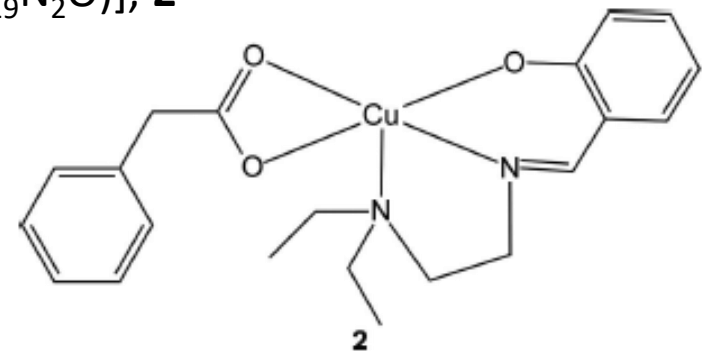
In structures such as this, nowadays most H atoms are placed in calculated positions, based on the environment and perceived hybridization of the C atoms to which they are bonded.

What would CheckCIF find if we were to make the simple mistake of putting just one H atom (AFIX 43) on C12 instead of the two (AFIX 23) that should be there?

A hydrogen-atom issue



[(E)-2-({[2-(**diethylamino**)ethyl]imino}methyl)phenolato-κ^3N,N',O](2-phenylacetato-κ^2O,O')copper(II), $[Cu(C_8H_7O_2)(C_{13}H_{19}N_2O)]$, **2**



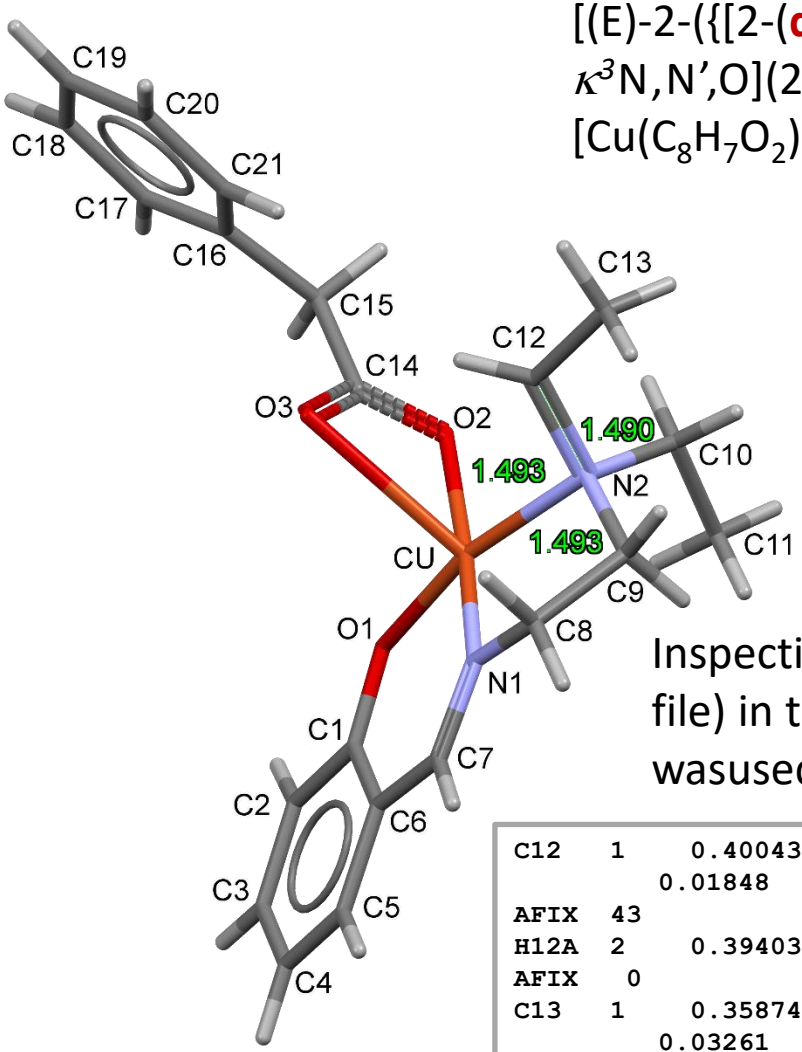
We get a warning that there is negative difference density on this H atom (H12A). It is significant that this warning appears ONLY for this H atom.

PLAT977_ALERT_2_C Check Negative Difference Density on H12A -0.44 eA-3

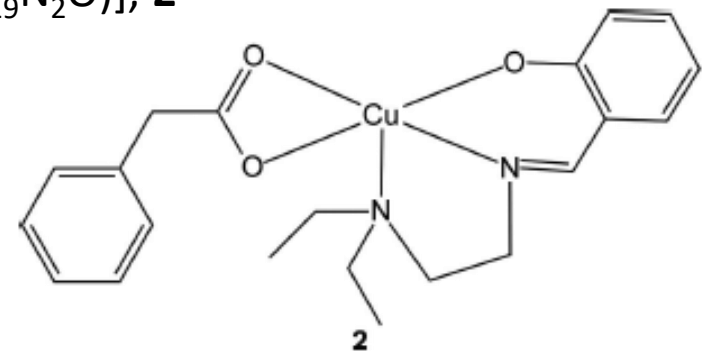
Also, we might notice that the formula that appears in the text and Table 1 has one more H than the formula derived from the atoms in the CIF.

Sum formula	C21 H25 Cu N2 O3	C21 H25 Cu N2 O3

A hydrogen-atom issue



[(E)-2-({[2-(**diethylamino**)ethyl]imino}methyl)phenolato-κ^3N,N',O](2-phenylacetato-κ^2O,O')copper(II), $[Cu(C_8H_7O_2)(C_{13}H_{19}N_2O)]$, **2**



Inspection of the embedded instruction file (ShelxL .res file) in the CIF reveals that AFIX 43, rather than AFIX 23, wasused for C12. This is easily corrected.

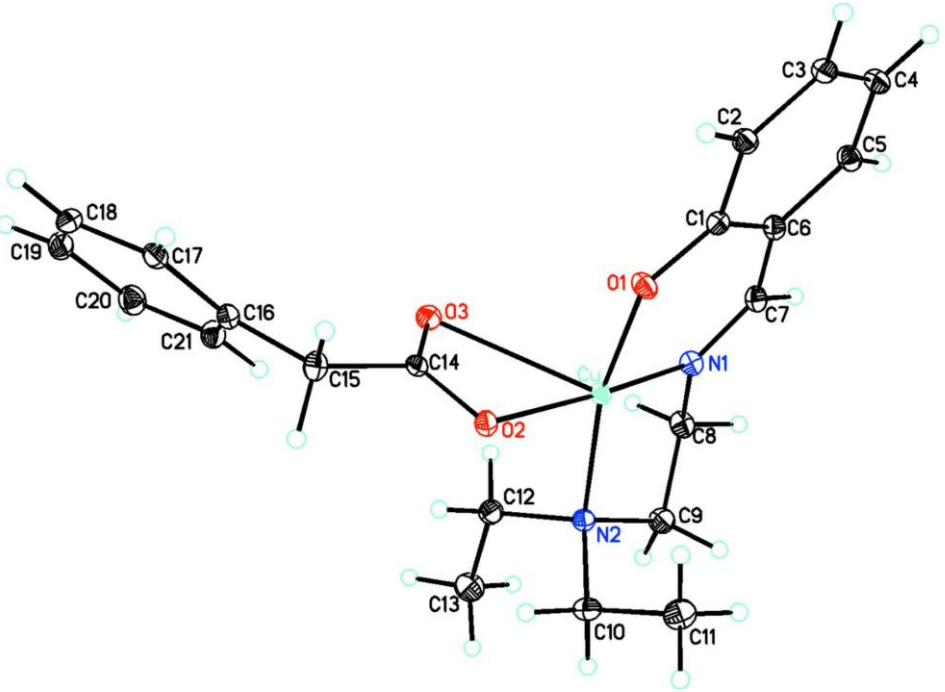
```
C12    1    0.400436    0.437307    0.632520    11.00000    0.02036    0.03152 =
         0.01848    0.00373   -0.00136   -0.00700
AFIX  43
H12A   2    0.394039    0.468526    0.562860    11.00000   -1.20000
AFIX   0
C13    1    0.358745    0.304857    0.692848    11.00000    0.02605    0.03757 =
         0.03261    0.00417    0.00321   -0.01144
AFIX 137
...
AFIX   0
```

A hydrogen-atom issue

[(E)-2-({[2-(**diethylamino**)ethyl]imino}methyl)phenolato-κ^3N,N',O](2-phenylacetato-κ^2O,O')copper(II),
$[Cu(C_8H_7O_2)(C_{13}H_{19}N_2O)]$, **2**

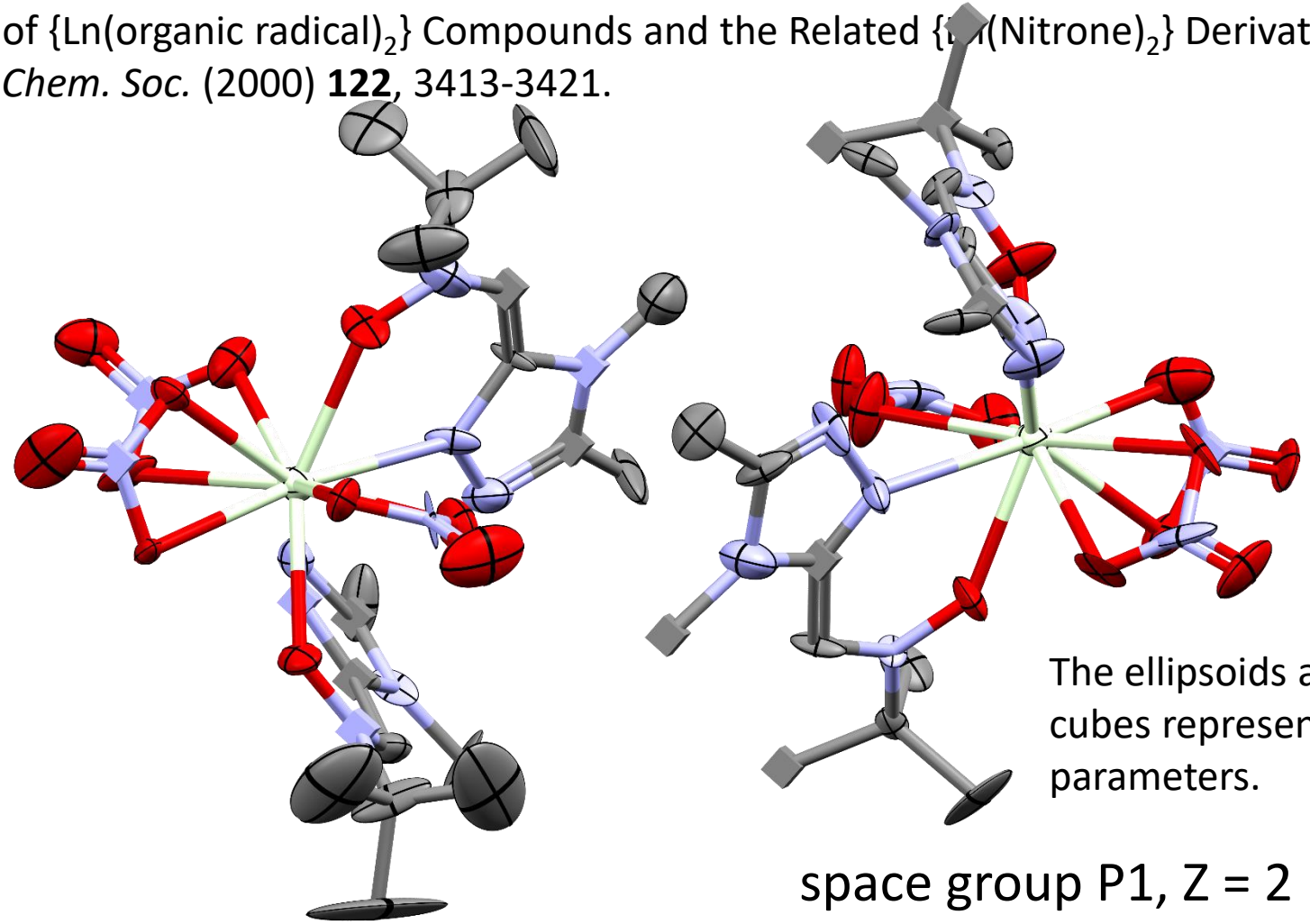
In many cases these issues arise before publication and are corrected by the time the structure is published. In this case the published structure is correct.

Acta Cryst. (2019) **C75,** 538-544. doi: 10.1107/S2053229619003267
The crystal and molecular structures of three copper-containing complexes and their activities in mimicking galactose oxidase.



Missed symmetry example

Kahn, M. L., Sutter, J.-P., Golhen, S., Guionneau, P., Ouahab,, L., Kahn, O. & Chasseau, D. Systematic Investigation of the Nature of The Coupling between a Ln(III) Ion (Ln) Ce(III) to Dy(III)) and Its Aminoxyl Radical Ligands. Structural and Magnetic Characteristics of a Series of {Ln(organic radical)$_2$} Compounds and the Related {Ln(Nitrone)$_2$} Derivatives *J. Am. Chem. Soc.* (2000) **122**, 3413-3421.



The ellipsoids are unusual. cubes represent NPD parameters.

space group P1, Z = 2

Missed symmetry example

CheckCIF indicates that something is wrong.

Alert level A

…
LABEL01_ALERT_1_A An _atom_site_label occurs more than once in the atom list. H9D
LABEL01_ALERT_1_A An _atom_site_label occurs more than once in the atom list. H9E
LABEL01_ALERT_1_A An _atom_site_label occurs more than once in the atom list. H9F
PLAT070_ALERT_1_A Duplicate Atomic Label on INPUT ..... H9D Note
And 2 other PLAT070 Alerts More ...
PLAT211_ALERT_2_A ADP of Atom N13 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C2 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C4 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C8 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C10 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C11 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C13 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C17 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom N101 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom N105 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom N108 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom N111 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom N112 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C101 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C105 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C115 is N.P.D. or (nearly) 2D . Please Check
PLAT211_ALERT_2_A ADP of Atom C117 is N.P.D. or (nearly) 2D . Please Check
PLAT213_ALERT_2_A Atom O5 has ADP max/min Ratio ..... 7.4 oblate
PLAT213_ALERT_2_A Atom N5 has ADP max/min Ratio ..... 7.5 oblate
PLAT213_ALERT_2_A Atom C7 has ADP max/min Ratio ..... 5.5 oblate
PLAT213_ALERT_2_A Atom N106 has ADP max/min Ratio ..... 7.0 prolat
PLAT213_ALERT_2_A Atom N113 has ADP max/min Ratio ..... 8.5 prolat
PLAT213_ALERT_2_A Atom C112 has ADP max/min Ratio ..... 7.9 prolat
PLAT213_ALERT_2_A Atom C116 has ADP max/min Ratio ..... 5.4 oblate

J. Am. Chem. Soc. (2000) **122**, 3413-3421.

Missed symmetry example

CheckCIF indicates that something is wrong.

Alert level B

PLAT029_ALERT_3_B _diffrn_measured_fraction_theta_full value Low . 0.952 Why?
PLAT111_ALERT_2_B ADDSYM Detects New (Pseudo) Centre of Symmetry . 100 %Fit
PLAT113_ALERT_2_B ADDSYM Suggests Possible Pseudo/New Space Group P-1 Check
PLAT213_ALERT_2_B Atom O6 has ADP max/min Ratio ..... 4.6 oblate
And 3 other PLAT213 Alerts Less ...
PLAT213_ALERT_2_B Atom N4 has ADP max/min Ratio ..... 4.4 oblate
PLAT213_ALERT_2_B Atom C110 has ADP max/min Ratio ..... 4.4 prolat
PLAT213_ALERT_2_B Atom C111 has ADP max/min Ratio ..... 4.7 prolat
PLAT220_ALERT_2_B Non-Solvent Resd 2 C Ueq(max)/Ueq(min) Range 8.4 Ratio
PLAT234_ALERT_4_B Large Hirshfeld Difference O5 --N11 . 0.26 Ang.
And 2 other PLAT234 Alerts More ...
PLAT242_ALERT_2_B Low 'MainMol' Ueq as Compared to Neighbors of C110 Check
PLAT342_ALERT_3_B Low Bond Precision on C-C Bonds ..... 0.0395 Ang.
PLAT369_ALERT_2_B Long C(sp2)-C(sp2) Bond C114 - C115 . 1.61 Ang.

Here, among lots of alerts related to the displacement parameters, is the alert about higher symmetry.

… and lots of C-level alerts involving the displacement parameters.

J. Am. Chem. Soc. (2000) **122**, 3413-3421.

Missed symmetry example

CheckCIF indicates that something is wrong.
There are alerts at every level related to the displacement parameters.

Alert level C

SHFSU01_ALERT_2_C The absolute value of parameter shift to su ratio > 0.05 Absolute value of the parameter shift to su ratio given 0.091 Additional refinement cycles may be required.
PLAT036_ALERT_1_C No s.u. Given for Flack Parameter ..... Please Do !
PLAT052_ALERT_1_C Info on Absorption Correction Method Not Given Please Do !
PLAT080_ALERT_2_C Maximum Shift/Error ..... 0.09 Why ?
PLAT090_ALERT_3_C Poor Data / Parameter Ratio (Zmax > 18) ..... 6.72 Note
PLAT213_ALERT_2_C Atom O11 has ADP max/min Ratio ..... 3.2 oblate
And 12 other PLAT213 Alerts More ...
PLAT220_ALERT_2_C Non-Solvent Resd 1 C Ueq(max)/Ueq(min) Range 4.0 Ratio
And 2 other PLAT220 Alerts More ...
PLAT222_ALERT_3_C Non-Solv. Resd 1 H Uiso(max)/Uiso(min) Range 4.3 Ratio
PLAT222_ALERT_3_C Non-Solv. Resd 2 H Uiso(max)/Uiso(min) Range 6.4 Ratio
PLAT230_ALERT_2_C Hirshfeld Test Diff for O12 --N13 . 5.5 s.u. PLAT234_ALERT_4_C Large Hirshfeld Difference Pr2 --O12 . 0.20 Ang.
And 26 other PLAT234 Alerts More ...
PLAT241_ALERT_2_C High 'MainMol' Ueq as Compared to Neighbors of O1 Check
And 5 other PLAT241 Alerts More ...
PLAT242_ALERT_2_C Low 'MainMol' Ueq as Compared to Neighbors of Pr2 Check
And 7 other PLAT242 Alerts

J. Am. Chem. Soc. (2000) **122**, 3413-3421.

Missed symmetry example

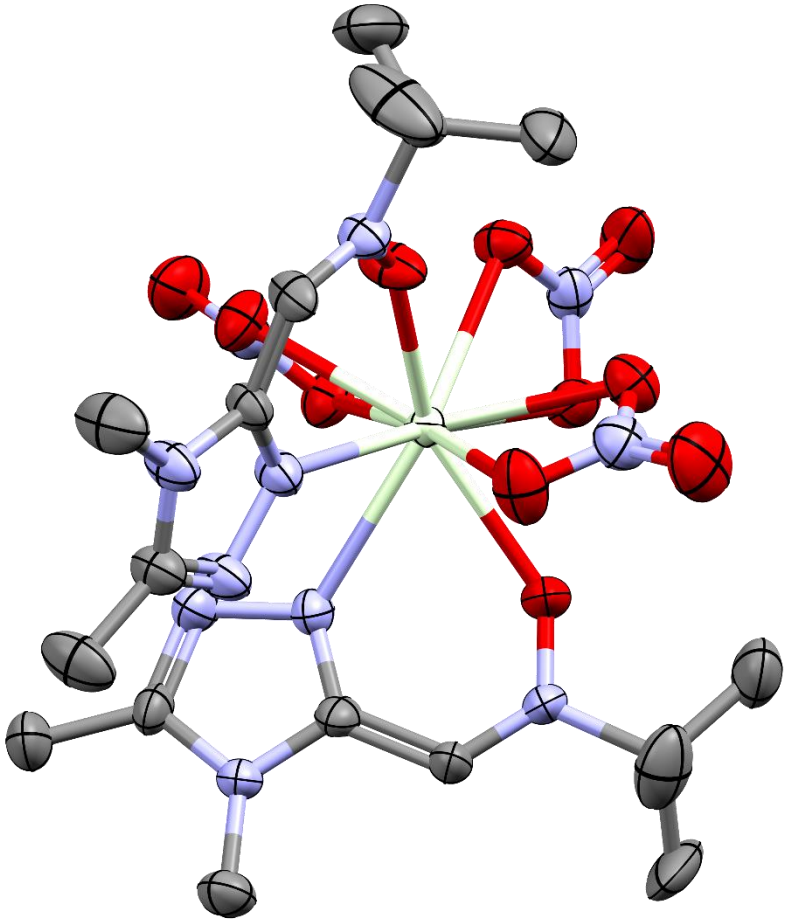
All the evidence leads us to the conclusion that we have higher symmetry.
We can solve the structure again using space group P(-1), or we can ask Platon to make the change for us (ADDSYM function).

```
Cell Lattice  a       b       c    Alpha   Beta  Gamma Volume CrystalSystem Laue
-------------------------------------------------------------------------------
Input   aP 10.199  10.630  14.062  82.49  69.36  83.35   1410    triclinic    -1
Reduced  P 10.199  10.630  14.062  82.49  69.36  83.35   1410
Convent aP 10.199  10.630  14.062  82.49  69.36  83.35   1410    triclinic    -1
                                                          "Pr(Nitrone"  PLATON-ADDSYM    Page    3
================================================================================================================================

          Conventional, New or Pseudo Symmetry
================================================================================

Space Group  H-M:  P-1                                        Laue:   -1
Space Group Hall: -P 1                                [Schoenflies: Ci^1  ]
Lattice Type: aP,  Centric,    Triclinic, Multiplicity:   2( 1), No:   2

  Nr            ***** Symmetry Operation(s) *****

   1              X ,             Y ,             Z
   2            - X ,           - Y ,           - Z

:: Origin Shifted to: 0.1919, 0.1874, 0.2457 after Transformation

::                      (  1.0000  0.0000  0.0000) ( -0.1919)
:: R/t for Coordinates  (  0.0000  1.0000  0.0000) ( -0.1874)
::                      (  0.0000  0.0000  1.0000) ( -0.2457)

:: - Symmetry Elements Preceded by an Asterisk are New and Indicate
::   Missed/Pseudosymmetry.:: - Proposed Inversion or (Glide) Planes do NOT Apply
::   for Chiral Molecules.
:: - Glide Plane Codes are with Reference to the Input Cell !!

P! Pr(NitronP1         aP=>aP 1.0 0.000 0.00 0.500 1.00   100% P-1
```

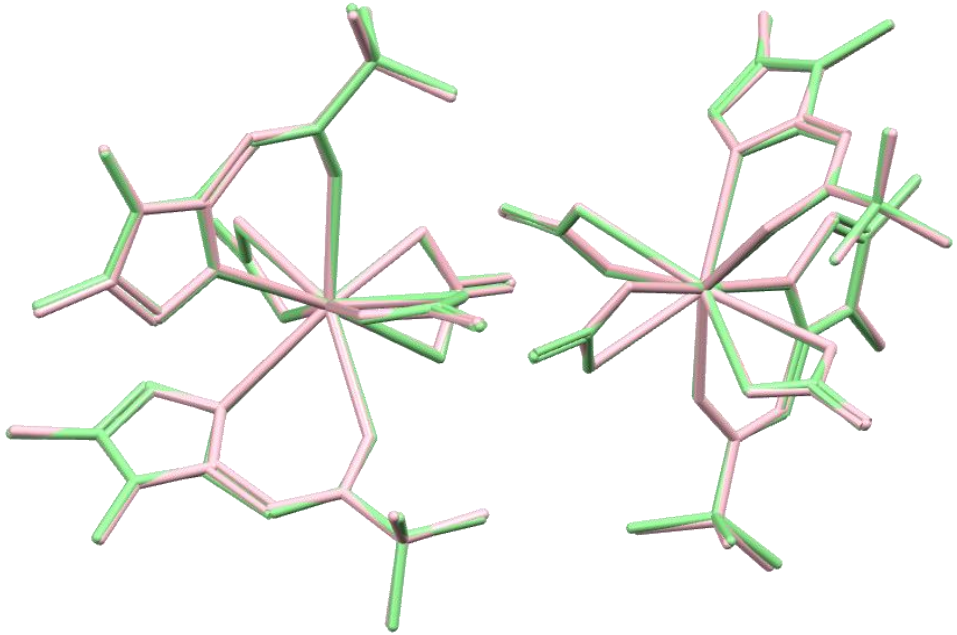
And if we use ADDSYM-SHX, Platon will write a Shelx-style .res file with a model based on the new space group.

Missed symmetry example; displacement and geometry

Kahn, M. L., Sutter, J.-P., Golhen, S., Guionneau, P., Ouahab,, L., Kahn, O. & Chasseau, D. *J. Am. Chem. Soc.* (2000) **122**, 9566.
New description in the centric group P(-1).



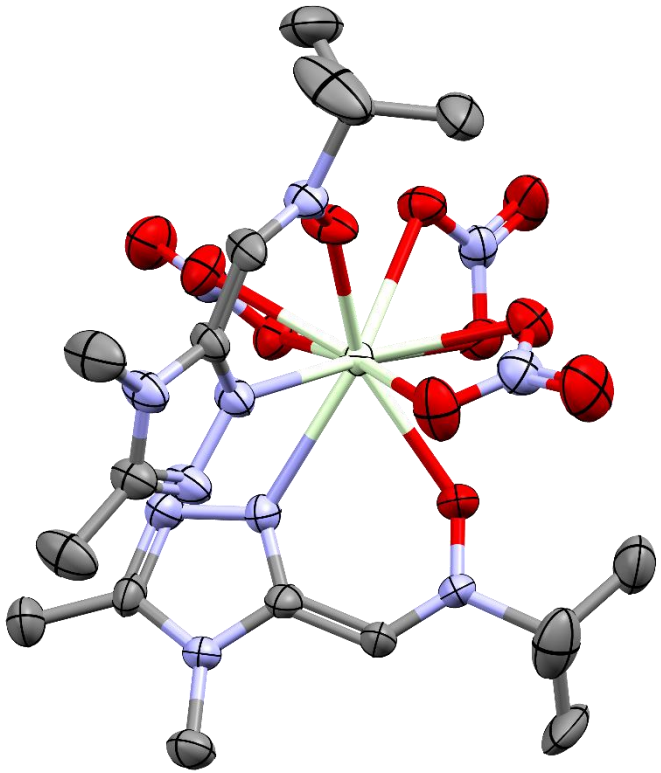
This is much better.



Overlay of the molecule from the new P(-1) refinement (pink) with molecule 1 (left) and molecule 2 (right) of the original P1 refinement (green).

Missed symmetry example; displacement and geometry

Kahn, M. L., Sutter, J.-P., Golhen, S., Guionneau, P., Ouahab,, L., Kahn, O. & Chasseau, D. *J. Am. Chem. Soc.* (2000) **122**, 9566. New description in the centric group P(-1).



This is much better.

Alert level A

EXPT005_ALERT_1_A _exptl_crystal_description is missing
Crystal habit description.
The following tests will not be performed.
CRYSR_01
DIFF003_ALERT_1_A _diffrn_measurement_device_type is missing
Diffractometer make and type. Replaces _diffrn_measurement_type.
PLAT183_ALERT_1_A Missing _cell_measurement_reflns_used Value .... Please Do !
PLAT184_ALERT_1_A Missing _cell_measurement_theta_min Value ..... Please Do !
PLAT185_ALERT_1_A Missing _cell_measurement_theta_max Value ..... Please Do !

Alert level B

PLAT029_ALERT_3_B _diffrn_measured_fraction_theta_full value Low . 0.952 Why?

Alert level C

PLAT052_ALERT_1_C Info on Absorption Correction Method Not Given Please Do !
PLAT213_ALERT_2_C Atom C91 has ADP max/min Ratio ..... 3.1 prolat
PLAT232_ALERT_2_C Hirshfeld Test Diff (M-X) Pr1 --O63 . 5.5 s.u.
PLAT241_ALERT_2_C High 'MainMol' Ueq as Compared to Neighbors of O58 Check
PLAT241_ALERT_2_C High 'MainMol' Ueq as Compared to Neighbors of O72 Check
PLAT242_ALERT_2_C Low 'MainMol' Ueq as Compared to Neighbors of Pr1 Check
And 3 other PLAT242 Alerts
More ...
PLAT342_ALERT_3_C Low Bond Precision on C-C Bonds ..... 0.0085 Ang.

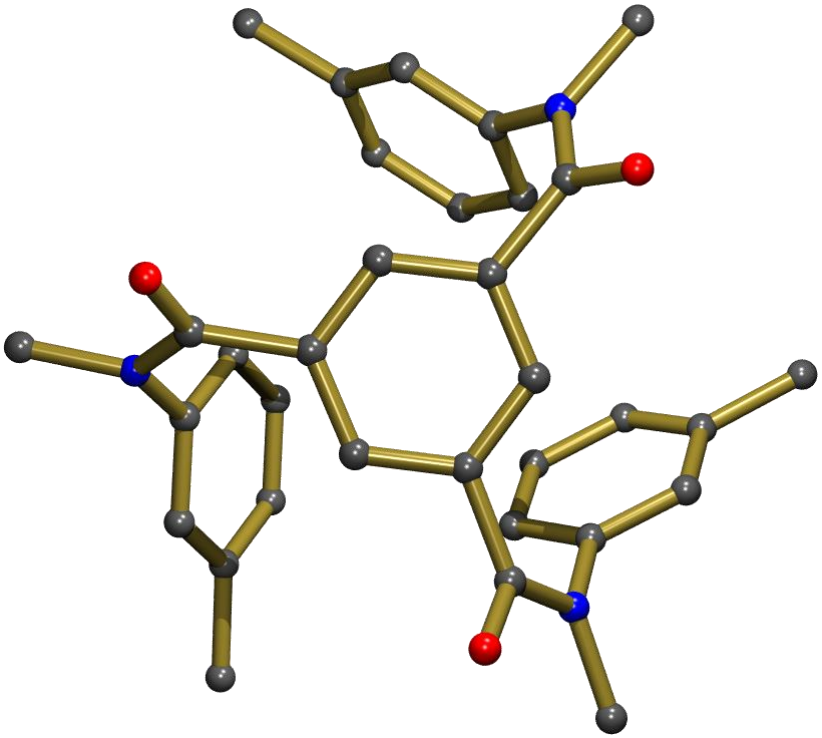
Alert level G

PLAT005_ALERT_5_G No Embedded Refinement Details Found in the CIF Please Do !
PLAT066_ALERT_1_G Predicted and Reported Tmin&Tmax Range Identical ? Check
PLAT093_ALERT_1_G No s.u.'s on H-positions, Refinement Reported as mixed Check
PLAT154_ALERT_1_G The s.u.'s on the Cell Angles are Equal ..(Note) 0.01 Degree
PLAT199_ALERT_1_G Reported _cell_measurement_temperature ..... (K) 293 Check
PLAT200_ALERT_1_G Reported _diffrn_ambient_temperature ..... (K) 293 Check
PLAT232_ALERT_2_G Hirshfeld Test Diff (M-X) Pr1 --O89 . 8.5 s.u.
PLAT794_ALERT_5_G Tentative Bond Valency for Pr1 (III) . 3.91 Info
PLAT899_ALERT_4_G SHELXL97 is Deprecated and Succeeded by SHELXL 2018 Note

Missed symmetry example - 2

Azumaya, I., Kagechika, H., Yamaguchi, K. & Shudo, K. (1995). *Tetrahedron* **51**, 5277-5290.
The structure in question is compound **6**. CSD refcode ZEMKIL.

	space group	*a*, Å	*b*, Å	*c*, Å	*V*, A^3	Z	R
$C_{33}H_{33}N_3O_3$	Pbca	17.862 (1)	17.863 (1)	17.816 (1)	5684 (2)	8	0.067



The molecule looks like it has a three-fold symmetry axis.

Herbstein, F. H. (1999). *Acta Cryst.* **C55**, 1196.
doi: 10.1107/S0108270198013924

Missed symmetry example - 2

Alert level A

EXPT005_ALERT_1_A _exptl_crystal_description is missing
Crystal habit description.
The following tests will not be performed.
CRYSR_01
DIFF003_ALERT_1_A _diffrn_measurement_device_type is missing
Diffractometer make and type. Replaces _diffrn_measurement_type.
ATOM007_ALERT_1_A _atom_site_aniso_label is missing
Unique label identifying the atom site.
GEOM001_ALERT_1_A _geom_bond_atom_site_label_1 is missing
Label identifying the atom site 1.
GEOM002_ALERT_1_A _geom_bond_atom_site_label_2 is missing
Label identifying the atom site 2.
GEOM003_ALERT_1_A _geom_bond_distance is missing
Distance between atom sites 1 and 2.
GEOM006_ALERT_1_A _geom_angle_atom_site_label_2 is missing
Label identifying the atom site 2.
GEOM007_ALERT_1_A _geom_angle_atom_site_label_3 is missing
Label identifying the atom site 3.
PLAT029_ALERT_3_A _diffrn_measured_fraction_theta_full value Low . 0.000 Why?
PLAT043_ALERT_1_A Calculated and Reported Mol. Weight Differ by .. 519.62 Check
PLAT046_ALERT_1_A Reported Z, MW and D(calc) are Inconsistent .... 0.000 Check
PLAT183_ALERT_1_A Missing _cell_measurement_reflns_used Value .... Please Do !
PLAT184_ALERT_1_A Missing _cell_measurement_theta_min Value ..... Please Do !
PLAT185_ALERT_1_A Missing _cell_measurement_theta_max Value ..... Please Do !
PLAT197_ALERT_1_A Missing _cell_measurement_temperature Datum .... Please Add
PLAT198_ALERT_1_A Missing _diffrn_ambient_temperature Datum .... Please Add
PLAT201_ALERT_2_A Isotropic non-H Atoms in Main Residue(s) ..... 39 Report
O1 O2 O3 N1 N2 N3 etc.
PLAT880_ALERT_1_A N0 datum for _diffrn_reflns_number ..... Please Do !
PLAT881_ALERT_1_A No Datum for _diffrn_reflns_av_R_equivalents ... Please Do !

Please note: When you use an old CIF, for example for a structure retrieved from the CSD, there may be a lot of information lacking in the CIF.

The alerts that are generated as a result of that, in this case, are not important.

We are interested in knowing about the symmetry.

No A-level alerts about symmetry!

Missed symmetry example - 2

Alert level B

PLAT112_ALERT_2_B ADDSYM Detects New (Pseudo) Symm. Elem 3 100 %Fit
And 3 other PLAT112 Alerts
More ...
PLAT113_ALERT_2_B ADDSYM Suggests Possible Pseudo/New Space Group Pa-3 Check
PLAT391_ALERT_3_B Deviating Methyl C24 H-C-H Bond Angle .... 100 Degree
PLAT391_ALERT_3_B Deviating Methyl C33 H-C-H Bond Angle .... 98 Degree

Alert level C

PLAT151_ALERT_1_C No s.u. (esd) Given on Volume ..... Please Do !
PLAT340_ALERT_3_C Low Bond Precision on C-C Bonds ..... 0.0043 Ang.
PLAT351_ALERT_3_C Long C-H (X0.96,N1.08A) C12 - H8 . 1.11 Ang.
PLAT351_ALERT_3_C Long C-H (X0.96,N1.08A) C22 - H19 . 1.11 Ang.
PLAT390_ALERT_3_C Deviating Methyl C15 X-C-H Bond Angle .... 116 Degree
And 2 other PLAT390 Alerts
More ...

Alert level G

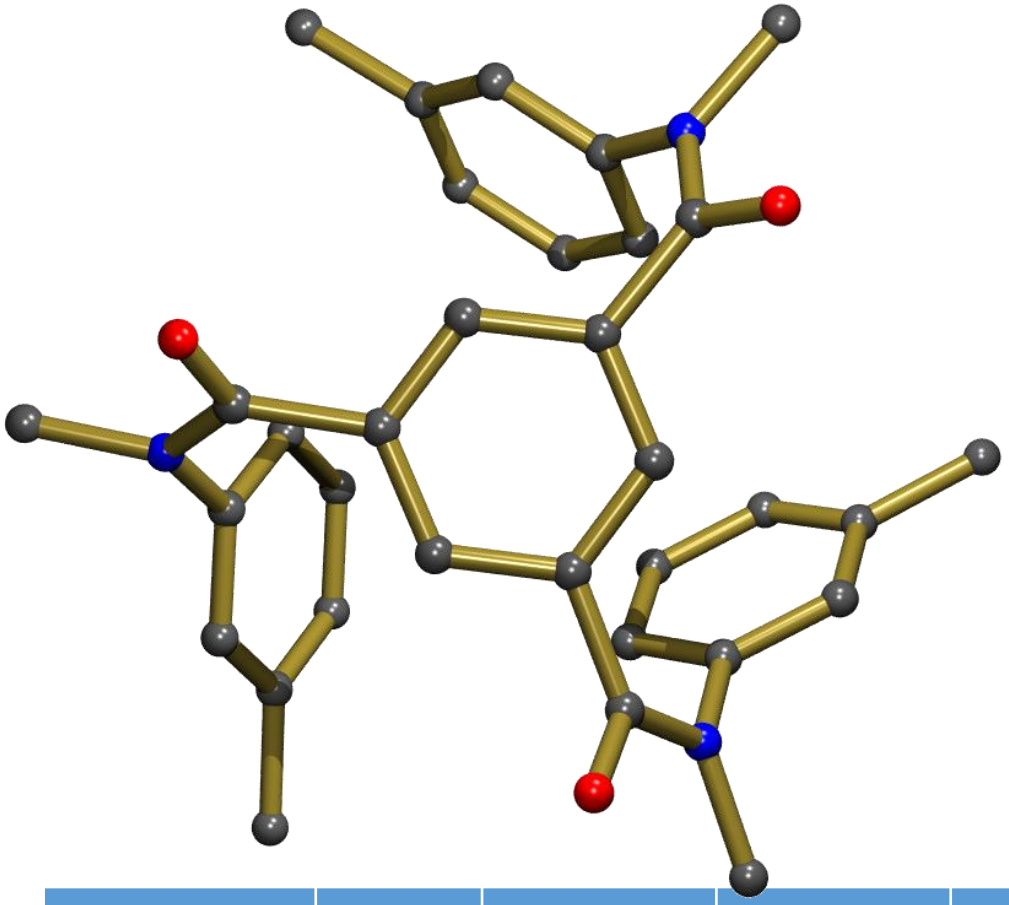
PLAT005_ALERT_5_G No Embedded Refinement Details Found in the CIF Please Do !
PLAT808_ALERT_5_G No Parseable SHELXL Style Weighting Scheme Found Please Check
PLAT882_ALERT_1_G No Datum for _diffrn_reflns_av_unetI/netI ..... Please Do !
PLAT883_ALERT_1_G No Info/Value for _atom_sites_solution_primary . Please Do !
PLAT981_ALERT_1_G No non-zero f" Anomalous Scattering Values Found Please Check
PLAT986_ALERT_1_G No non-zero f' Anomalous Scattering Values Found Please Check

Here it is!

For more recent structures, the CIF will have the diffraction data embedded within. So it would be possible for you to re-refine the structure in the new space group. For an older structure like this one, the reflection data are not present.

	space group	*a*, Å	*b*, Å	*c*, Å	*V*, A^3	Z	R
$C_{33}H_{33}N_3O_3$	Pbca	17.862 (1)	17.863 (1)	17.816 (1)	5684 (2)	8	0.067
	Pa(-3)	17.862 (1)				8	

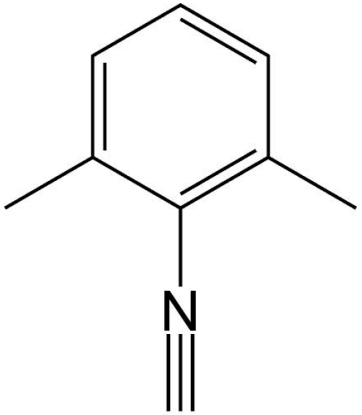
Missed symmetry example - 2



The molecule lies on a site of crystallographic symmetry 3. The multiplicity of the space group Pa(-3) is 24, so this gives Z = 8.

	space group	*a*, Å	*b*, Å	*c*, Å	*V*, A^3	Z	R
$C_{33}H_{33}N_3O_3$	Pbca	17.862 (1)	17.863 (1)	17.816 (1)	5684 (2)	8	0.067
	Pa(-3)	17.862 (1)				8	

Missed symmetry example - 3



2,6-dimethylphenylisocyanide, CNXyl

Ref.		space group	*a*, Å / α (°)	*b*, Å / β (°)	*c*, Å / γ (°)	*V*, A^3	Z	R
[1]	C_9H_9N	P(-1)	7.551 (1) 83.39 (2)	8.888 (2) 72.87 (1)	12.820 (2) 64.87 (1)	744.3 (2)	4	0.0621
	Platon	I2/a	14.580 89.99	7.551 113.41	14.735 90.00	1489	8	
[2]	C_9H_9N	I2/a	14.5535 (6) 90	7.5199 (2) 113.548 (5)	14.6333 (7) 90	1468.12 (11)	8	0.0397

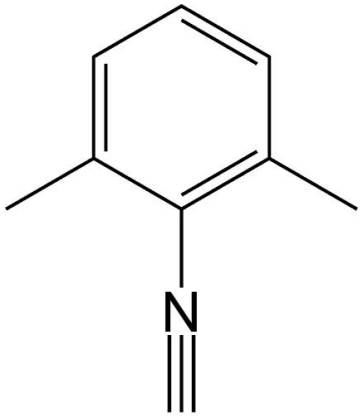
[1] Mathieson, T., Schier, A. & Schmidbaur, H. (2001). J. Chem. Soc., Dalton Trans. pp. 1196 – 1200. doi: 10.1039/b100117p Deposition CCDC 155748. Refcode EBONAK.

[2] Brennessel, W. W., Kucera, B. E., Young, V. G. Jr., Ellis, J. E. (2019). Acta Cryst. C75.

Missed symmetry example - 3

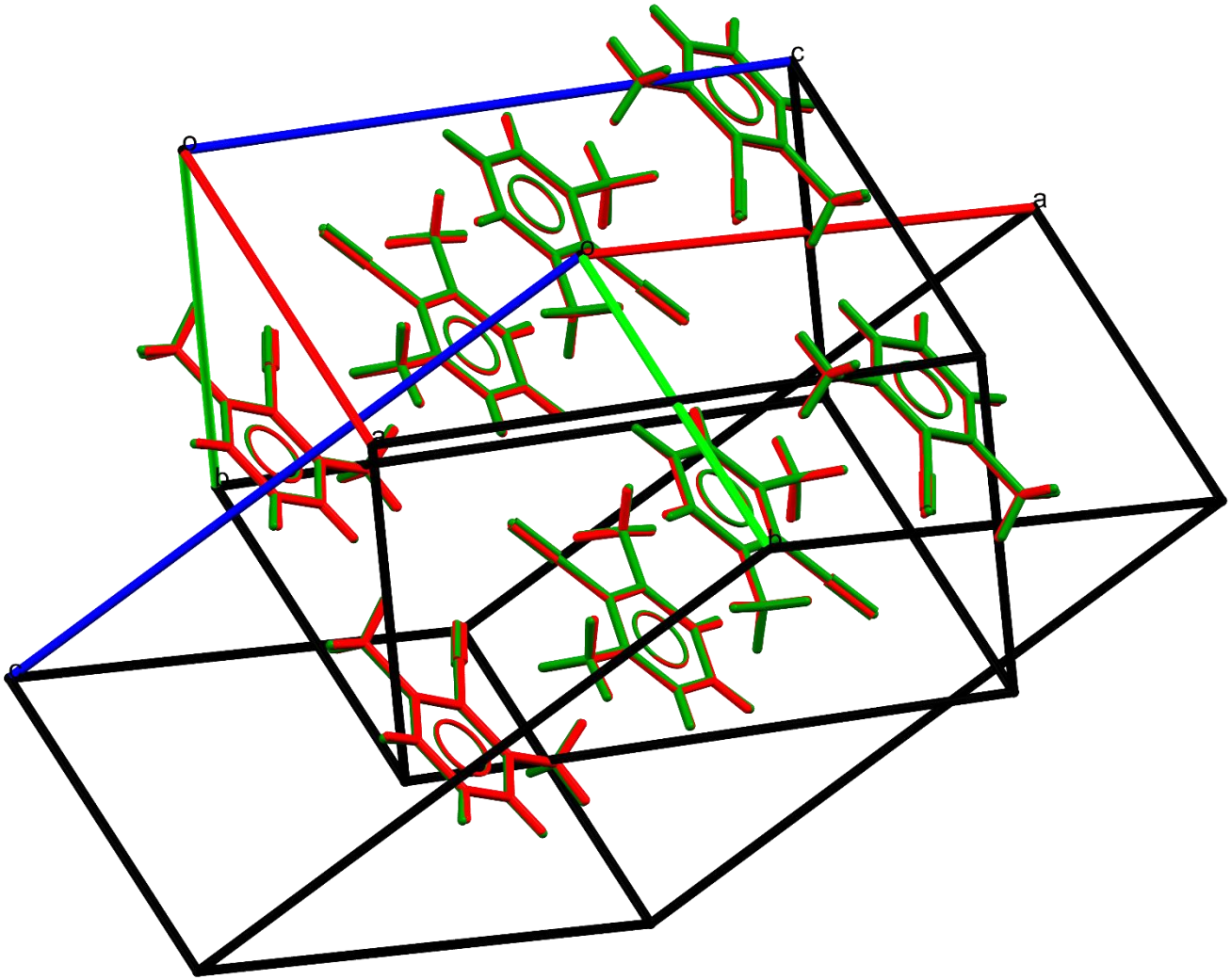
```
==========================================================================================================
ADDSYM - CHECK  (cf. MISSYM (C): Le Page, Y., J. Appl. Cryst. (1987), 20, 264-269; J. Appl. Cryst. (1988), 21,
983-984)
----------------------------------------------------------------------------------------------------------
- ADDSYM Search on ALL NON-H Chemical Types [Max NonFit 20 Perc]
- Number of Input Atoms Included in Search   20 (Unitcell   40)
- Density based on Input Atom Set = 1.170 g.cm-3 - Vol / Non-H atom = 18.6 Ang+3
- The Structure Implies the Following Symmetry Elements Subject to the Criteria:
- Criteria 1.00 Deg (Metric), 0.25 Ang (Rot), 0.45 Ang (Inv), 0.45 Ang (Transl)

Symm.  Input  Reduced  (Ang)        (Deg) Perc AvrDev.(Ang)          Input Cell
Elem Cell_Row Cell_Row   d  Typ Dot Angle Fit  MaxDev.             x     y     z
----------------------------------------------------------------------------
 n * [ 1 0 0] [ 1 0 0]  7.55  2  2  0.01  100   0.005  Through   1/4     0     0
                                    C7   -C9    0.008  Glide     1/2   1/2   1/2
              [ 1 0-2] 24.50  2  2  0.66               Metric

              [-1 2 0] 16.09  2  2  0.66               Metric

-1   ================================== 100       0  at          0     0     0

         T.R.A.N.S.F.O.R.M.A.T.I.O.N  M.A.T.R.I.X for CELL and HKL DATA
         ================================================================
   Reduced->Convent          Input->Reduced       T = Input->Convent:    a' = T a
-------------------------------------------------------------------------------
(     0     1    -1 )   (    -1     0     0 )   (     1    -1    -1 )     Det(T)
(    -1     0     0 ) X (     0    -1     0 ) = (     1     0     0 )       =
(    -1     1     1 )   (    -1     0     1 )   (     0    -1     1 )     2.000

Cell Lattice  a       b       c    Alpha   Beta  Gamma Volume CrystalSystem Laue
----------------------------------------------------------------------------
Input   aP  7.551   8.888  12.820  83.39  72.87  64.87    744    triclinic    -1
Reduced  P  7.551   8.888  12.820  82.24  72.87  64.87    744
Convent mI 14.580   7.551  14.735  89.99 113.41  90.00   1489   monoclinic   2/m
:: Cell Angles differ 0.01 Deg. from (90/120) "EBONAK"  PLATON-ADDSYM    Page    3
```

Missed symmetry example - 3



Green: EBONAK
Red: Brennessel *et al.*

The results of the two analyses overlap very well.

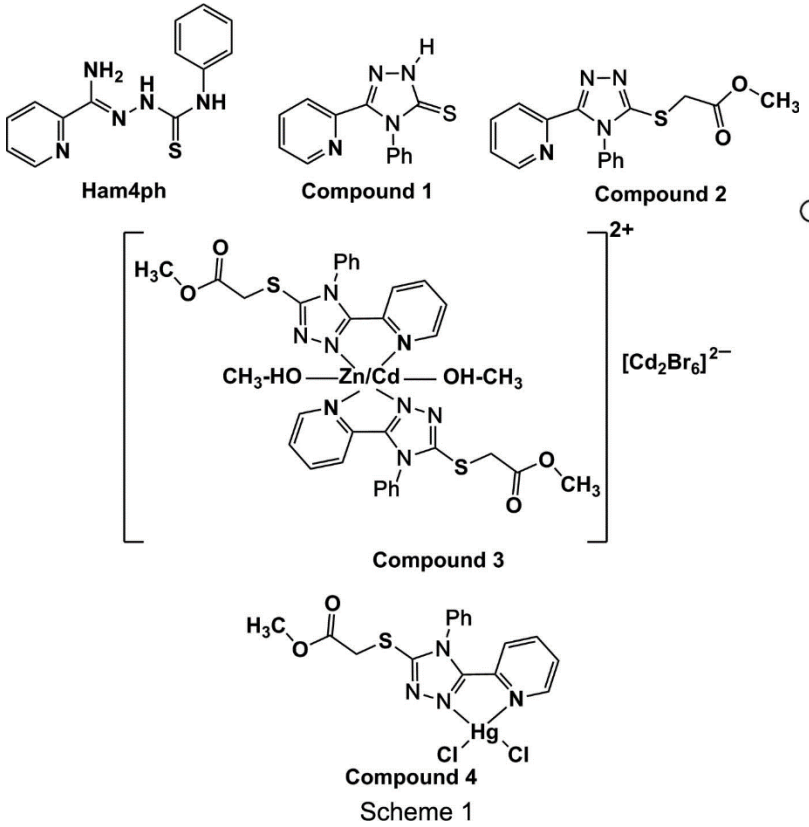


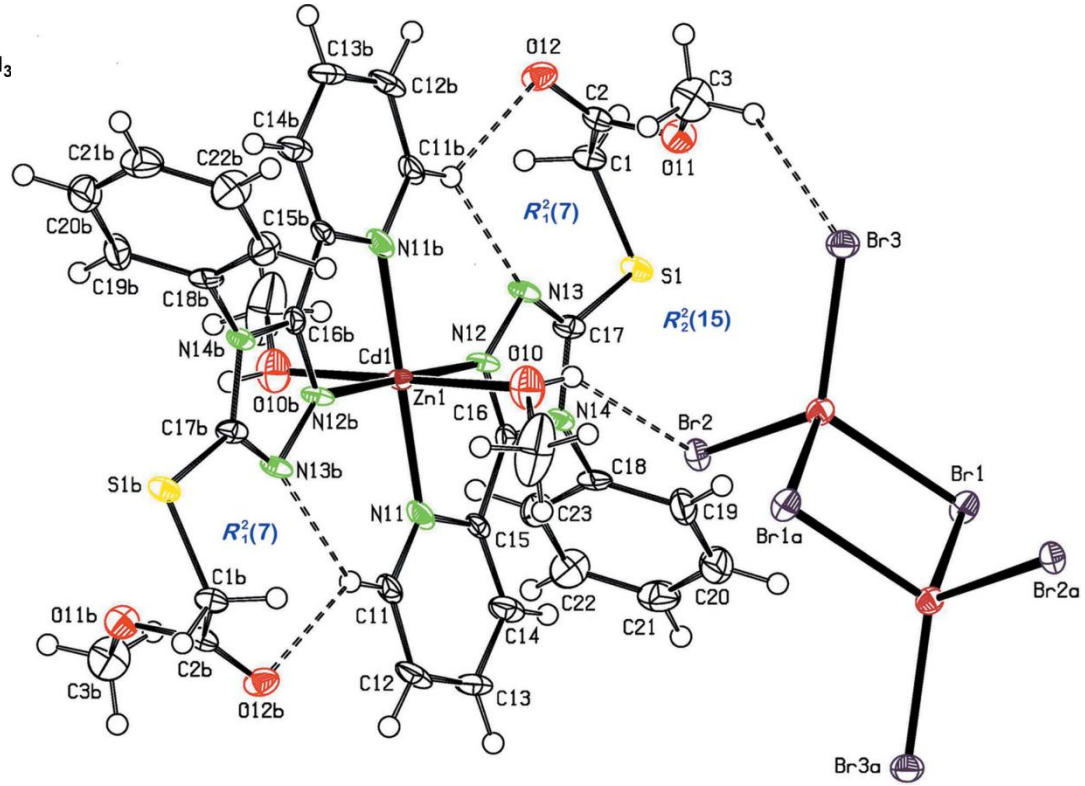
[1] Mathieson, T., Schier, A. & Schmidbaur, H. (2001). J. Chem. Soc., Dalton Trans. pp. 1196 – 1200. doi: 10.1039/b100117p Deposition CCDC 155748. Refcode EBONAK.

[2] Brennessel, W. W., Kucera, B. E., Young, V. G. Jr., Ellis, J. E. (2019). Acta Cryst. C75.

CheckCIF as an aid during structure solution and refinement

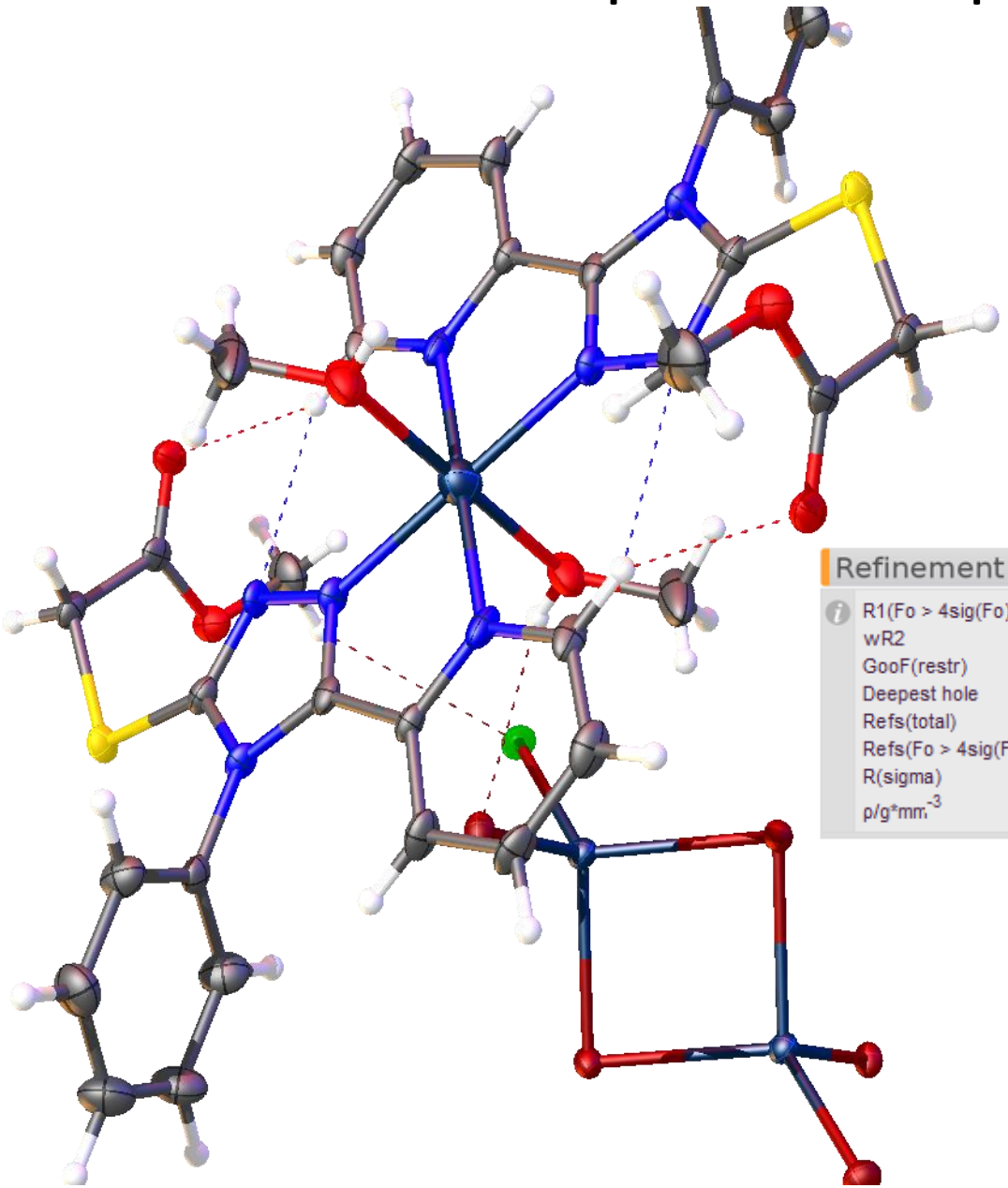
Design and synthesis of methyl 2-{[4-phenyl-5-(pyridin-2-yl)-4H-1,2,4-triazol-3 yl]sulfanyl}acetate (phpy2NS) as ligand for complexes of Group 12 elements: structural assessment and hydrogen-bonded supramolecular assembly analysis
Alfonso Castiñeiras, Isabel García-Santos and Manuel Saa (2019). Acta Cryst. C75, 891-903.
doi: 10.1107/S2053229619006820X





From the preparation, it was expected to be a Cd compound – no other d-block element.

Cd model – displacement parameters



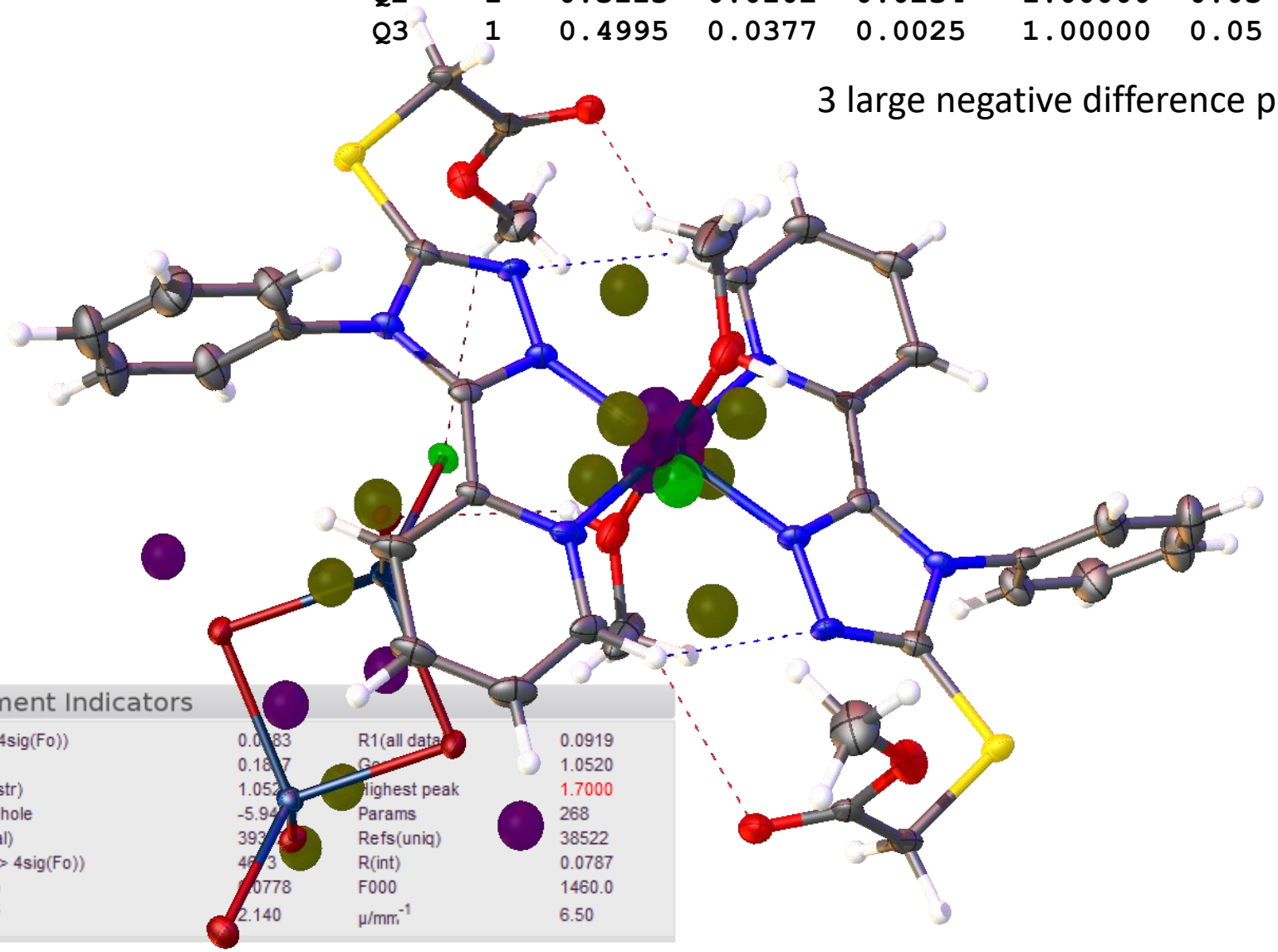
Refinement Indicators

R1(Fo > 4sig(Fo))	0.0583	R1(all data)	0.0919
wR2	0.1817	GooF	1.0520
GooF(restr)	1.0520	Highest peak	1.7000
Deepest hole	-5.9400	Params	268
Refs(total)	39302	Refs(uniq)	38522
Refs(Fo > 4sig(Fo))	4673	R(int)	0.0787
R(sigma)	0.0778	F000	1460.0
ρ/g*mm^{-3}	2.140	μ/mm^{-1}	6.50

Cd model – difference Fourier map

Q1	1	0.4620	0.0047	0.0099	1.00000	0.05	-5.94
Q2	1	0.5113	-0.0102	0.0234	1.00000	0.05	-5.43
Q3	1	0.4995	0.0377	0.0025	1.00000	0.05	-4.87

3 large negative difference peaks



Refinement Indicators

R1(Fo > 4sig(Fo))	0.0[illegible]83	R1(all data)	0.0919
wR2	0.18[illegible]7	Ge[illegible]	1.0520
GooF(restr)	1.052	Highest peak	1.7000
Deepest hole	-5.94	Params	268
Refs(total)	393[illegible]	Refs(uniq)	38522
Refs(Fo > 4sig(Fo))	46[illegible]3	R(int)	0.0787
R(sigma)	[illegible]0778	F000	1460.0
ρ/g*mm^{-3}	2.140	μ/mm^{-1}	6.50

Cd model – CheckCIF

Alert level A

```
EXPT005_ALERT_1_A  _exptl_crystal_description is missing
           Crystal habit description.
           The following tests will not be performed.
           CRYSR_01
DIFF003_ALERT_1_A  _diffrn_measurement_device_type is missing
           Diffractometer make and type. Replaces _diffrn_measurement_type.
PLAT057_ALERT_3_A Correction for Absorption Required   RT(exp) ...      21.00 Do !
PLAT183_ALERT_1_A Missing _cell_measurement_reflns_used Value ....    Please Do !
PLAT184_ALERT_1_A Missing _cell_measurement_theta_min Value ......    Please Do !
PLAT185_ALERT_1_A Missing _cell_measurement_theta_max Value ......    Please Do !
```

unimportant!

Alert level B

```
DIFMN02_ALERT_2_B  The minimum difference density is < -0.1*ZMAX*1.00
           _refine_diff_density_min given =     -5.944
           Test value =     -4.800
PLAT098_ALERT_2_B Large Reported Min.  (Negative) Residual Density     -5.94 eA-3
```

important!

Alert level C

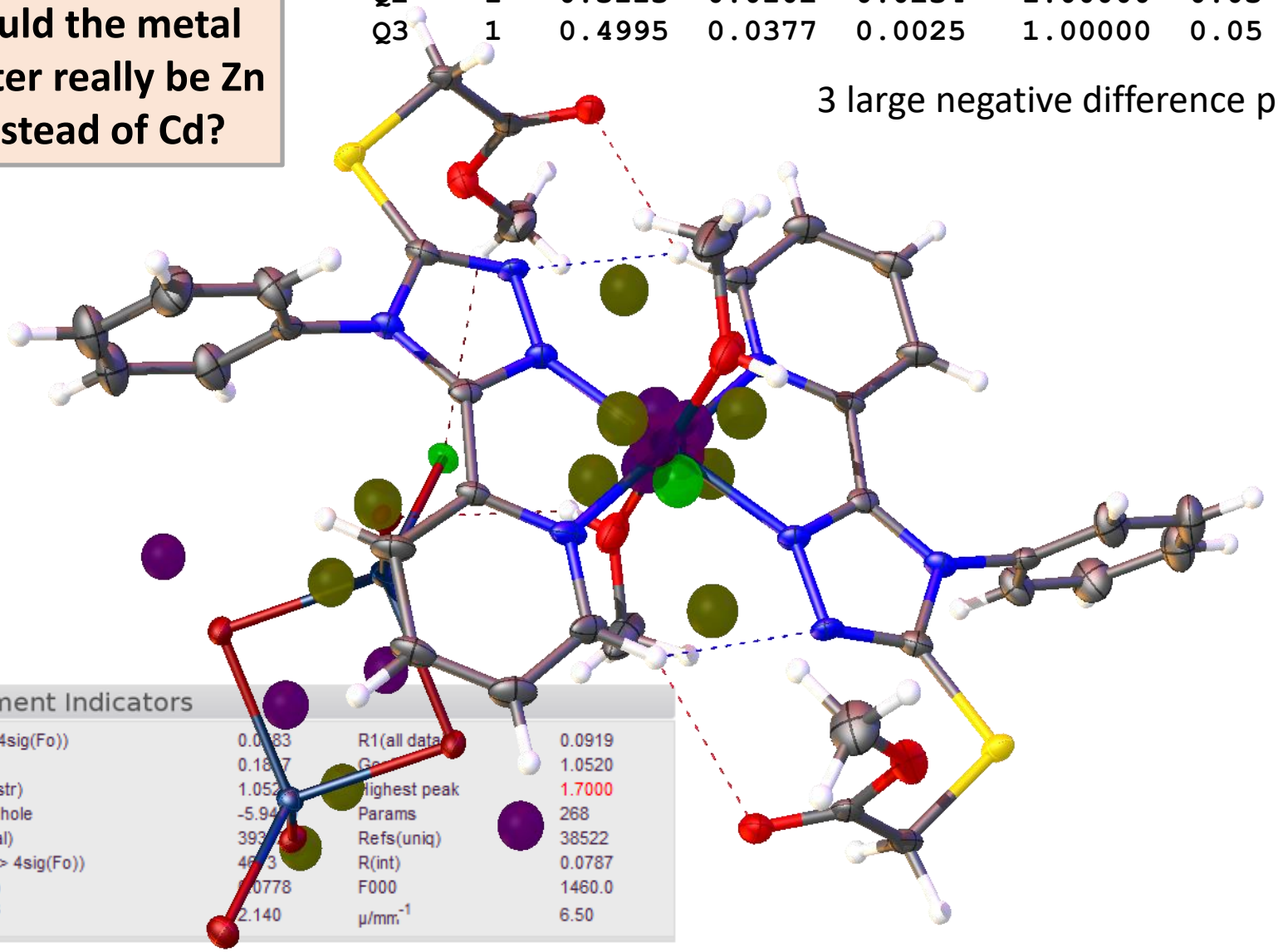
```
DIFMN03_ALERT_1_C  The minimum difference density is < -0.1*ZMAX*0.75
           The relevant atom site should be identified.
PLAT052_ALERT_1_C Info on Absorption Correction Method   Not Given     Please Do !
PLAT220_ALERT_2_C Non-Solvent  Resd 1  C   Ueq(max)/Ueq(min) Range       3.8 Ratio
PLAT342_ALERT_3_C Low Bond Precision on  C-C Bonds ..............      0.012 Ang.
```

Cd model – difference Fourier map

Q1	1	0.4620	0.0047	0.0099	1.00000	0.05	-5.94
Q2	1	0.5113	-0.0102	0.0234	1.00000	0.05	-5.43
Q3	1	0.4995	0.0377	0.0025	1.00000	0.05	-4.87

Could the metal center really be Zn instead of Cd?

3 large negative difference peaks

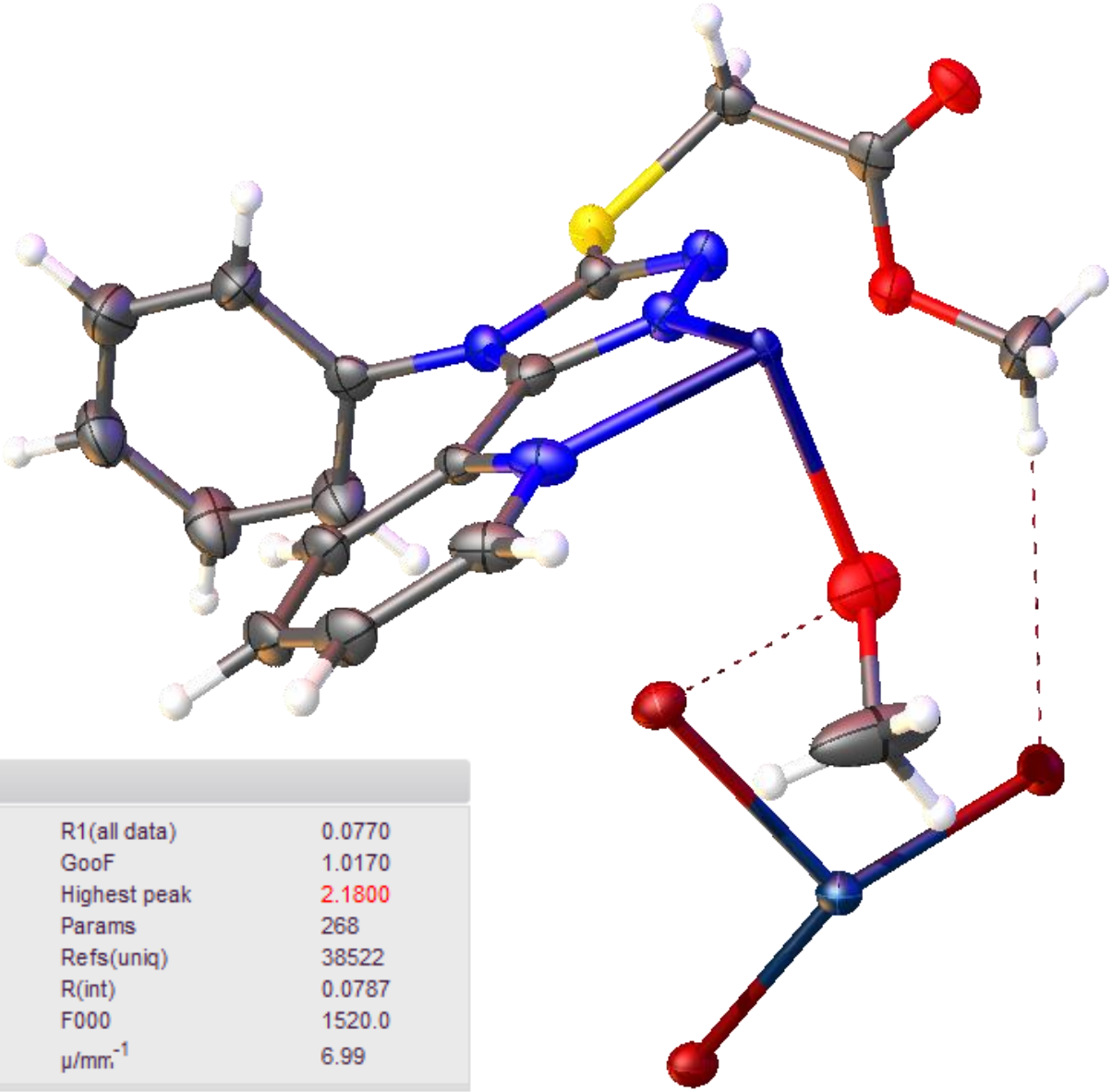


Refinement Indicators

R1(Fo > 4sig(Fo))	0.0[illegible]83	R1(all data)	0.0919
wR2	0.18[illegible]7	Ge[illegible]	1.0520
GooF(restr)	1.052	[illegible]ighest peak	1.7000
Deepest hole	-5.94	Params	268
Refs(total)	393[illegible]	Refs(uniq)	38522
Refs(Fo > 4sig(Fo))	4[illegible]3	R(int)	0.0787
R(sigma)	[illegible]0778	F000	1460.0
ρ/g*mm^{-3}	2.140	μ/mm^{-1}	6.50

Zn model – displacement parameters

When refined as Zn, the displacement parameters of the metal atom appear to be too small.



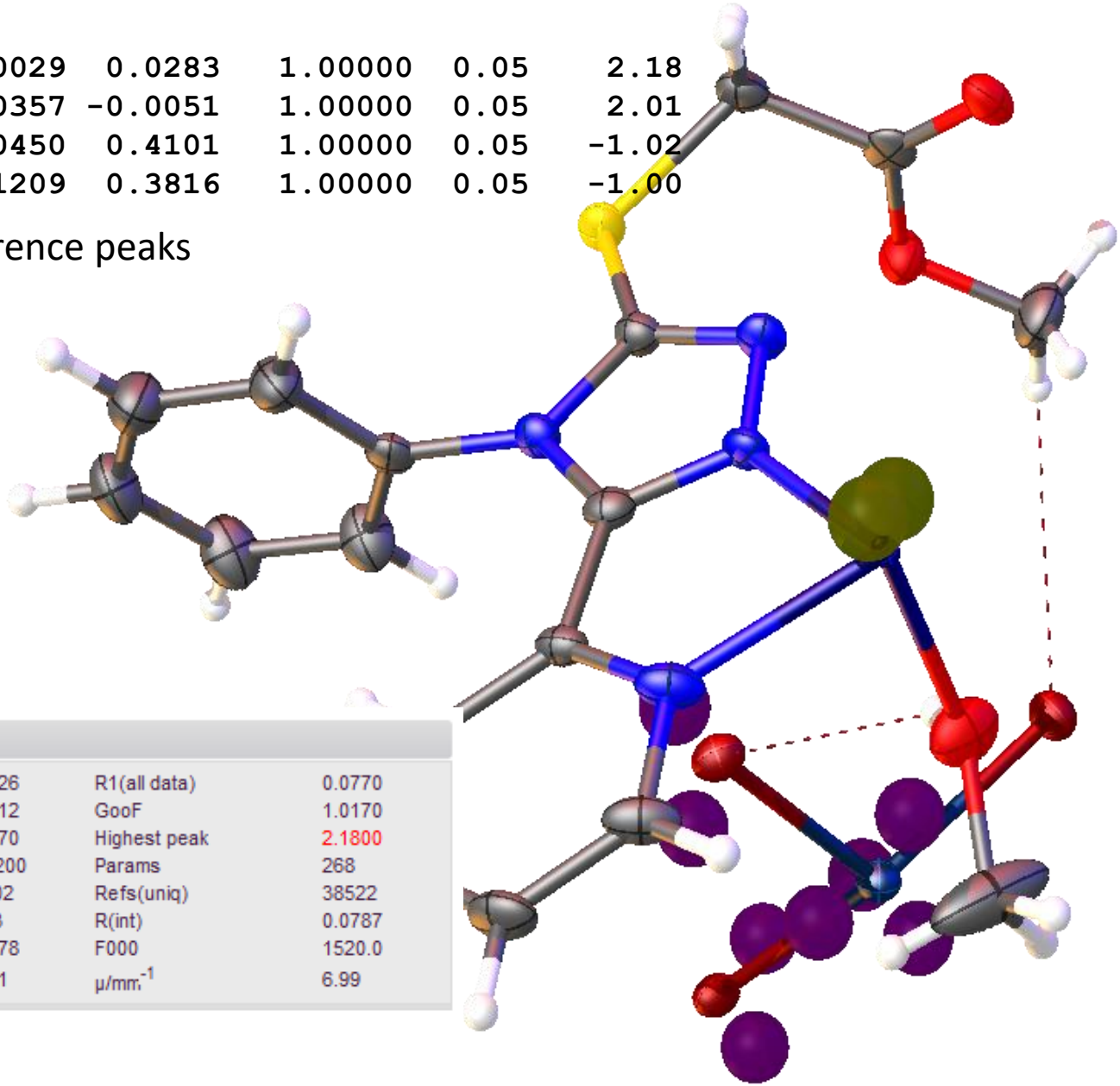
Refinement Indicators

R1(Fo > 4sig(Fo))	0.0426	R1(all data)	0.0770
wR2	0.1112	GooF	1.0170
GooF(restr)	1.0170	Highest peak	2.1800
Deepest hole	-1.0200	Params	268
Refs(total)	39302	Refs(uniq)	38522
Refs(Fo > 4sig(Fo))	4673	R(int)	0.0787
R(sigma)	0.0778	F000	1520.0
ρ/g*mm^{-3}	2.231	μ/mm^{-1}	6.99

Zn model – difference Fourier map

Q1	1	0.4855	0.0029	0.0283	1.00000	0.05	2.18
Q2	1	0.4982	0.0357	-0.0051	1.00000	0.05	2.01
Q3	1	0.4430	0.0450	0.4101	1.00000	0.05	-1.02
Q4	1	0.4623	0.1209	0.3816	1.00000	0.05	-1.00

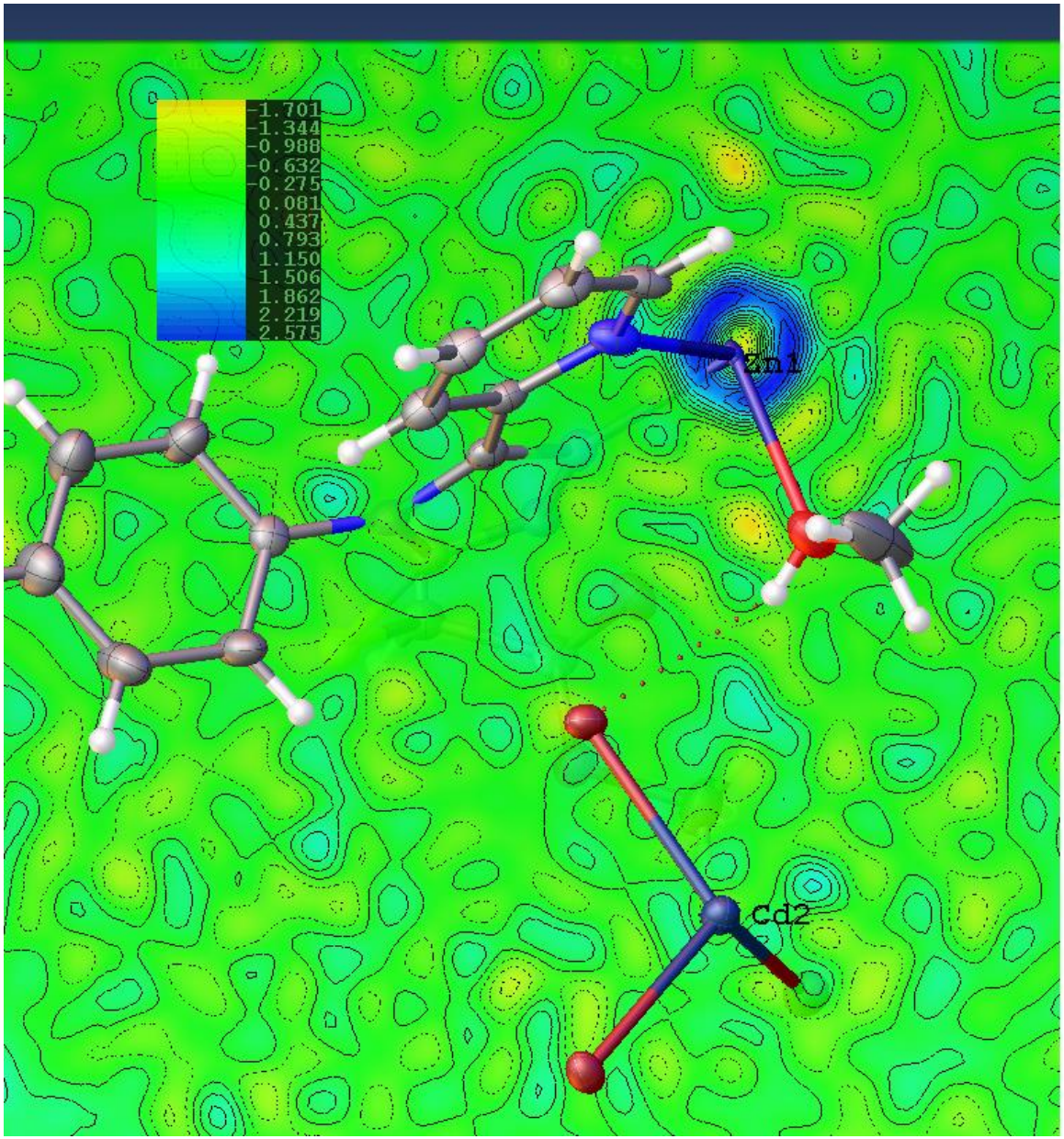
2 ‘large’ positive difference peaks



Refinement Indicators

R1(Fo > 4sig(Fo))	0.0426	R1(all data)	0.0770
wR2	0.1112	GooF	1.0170
GooF(restr)	1.0170	Highest peak	2.1800
Deepest hole	-1.0200	Params	268
Refs(total)	39302	Refs(uniq)	38522
Refs(Fo > 4sig(Fo))	4673	R(int)	0.0787
R(sigma)	0.0778	F000	1520.0
ρ/g*mm^{-3}	2.231	μ/mm^{-1}	6.99

Zn model – difference Fourier map
Useful Olex2 graphics



lg3239_sx_Zn

$P2_1/n$

E:\Acta-C\7proofs-2019-Feb-Julio\lg3239\Lwork\lg3239_sx_Zn.res

$C_{34}H_{36}Br_6Cd_3N_8O_6S_2Zn$

a = 11.4980(3)	α = 90°	Z = 2	R_1	4.26 %
b = 13.7848(4)	β = 93.4660(14)°	Z' = 0.5	wR_2	11.12 %
c = 15.0417(4)	γ = 90°	V = 2379.71(11)		

d min (Mo)	0.72	I/σ	12.9	Rint	7.87%	complete	100%
Shift	0.000	Max Peak	2.2	Min Peak	-1.0	GooF	1.017

Home | Work | View | Tools | Info

AutoChem 3.1

HARt

Images

Maps

View: contour+plane | Colours: 5 | min: -1.771 | max: 3.088 | Edit

Contours: 15

Map Scale: Scaled to Visible | Scaled to Full Map

Scale: 10 | 0 | Fix | 0

Depth: 0

Size: 15

Electron Density

Map: diff | Source: olex | Res/Å: 0.1 | Mask | Hide Map

Calculate Voids

Calculate Solvent Accessible Voids

Masks

Chemical Tools

Olex2 Constraints Restraints

Shelx Compatible Constraints

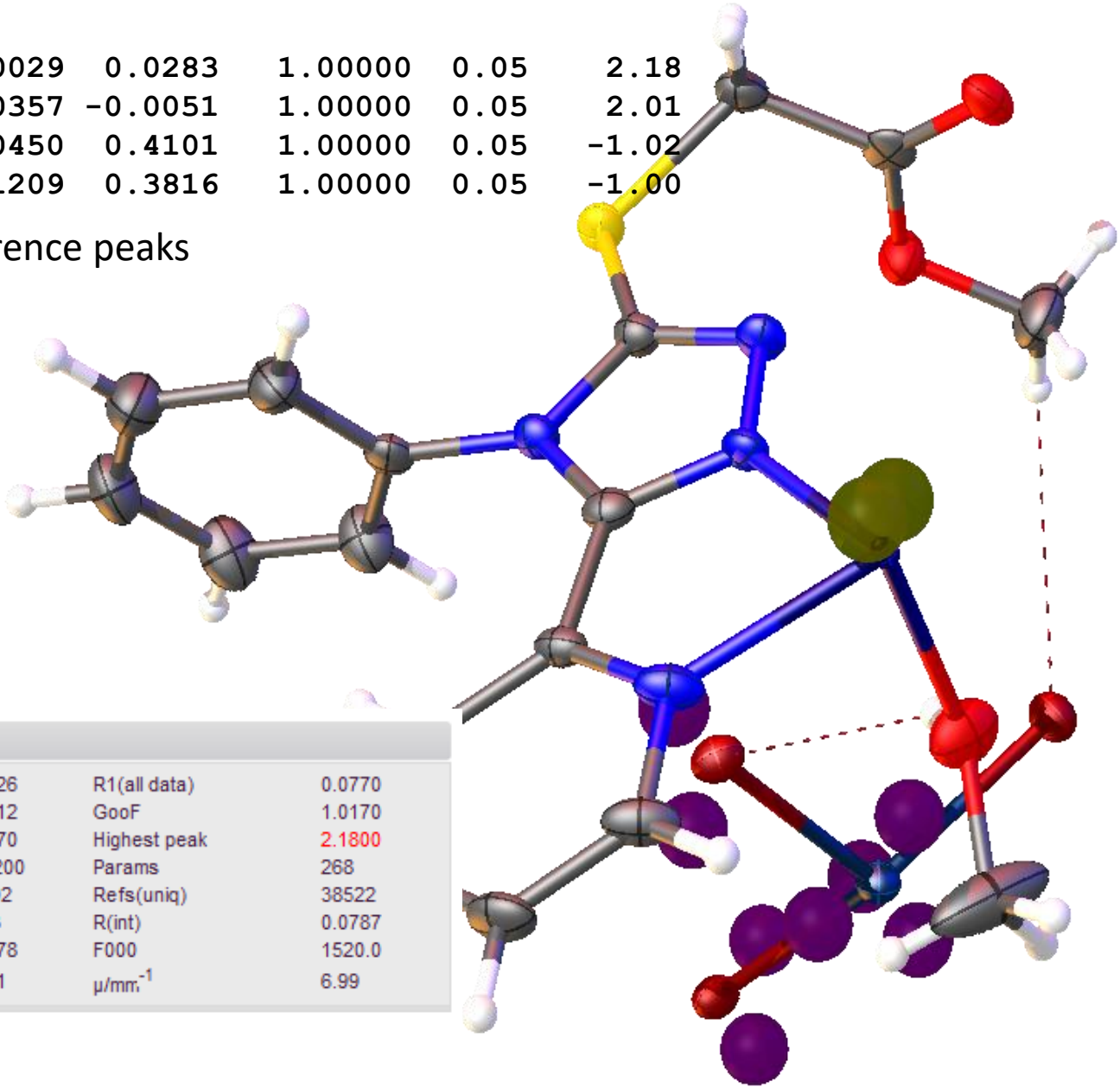
Shelx Compatible Restraints

Zn model – difference Fourier map

Q1	1	0.4855	0.0029	0.0283	1.00000	0.05	2.18
Q2	1	0.4982	0.0357	-0.0051	1.00000	0.05	2.01
Q3	1	0.4430	0.0450	0.4101	1.00000	0.05	-1.02
Q4	1	0.4623	0.1209	0.3816	1.00000	0.05	-1.00

2 ‘large’ positive difference peaks

Could the metal center really be a mixture of Cd and Zn?



Refinement Indicators

R1(Fo > 4sig(Fo))	0.0426	R1(all data)	0.0770
wR2	0.1112	GooF	1.0170
GooF(restr)	1.0170	Highest peak	2.1800
Deepest hole	-1.0200	Params	268
Refs(total)	39302	Refs(uniq)	38522
Refs(Fo > 4sig(Fo))	4673	R(int)	0.0787
R(sigma)	0.0778	F000	1520.0
ρ/g*mm^{-3}	2.231	μ/mm^{-1}	6.99

Zn model – CheckCIF

Alert level B

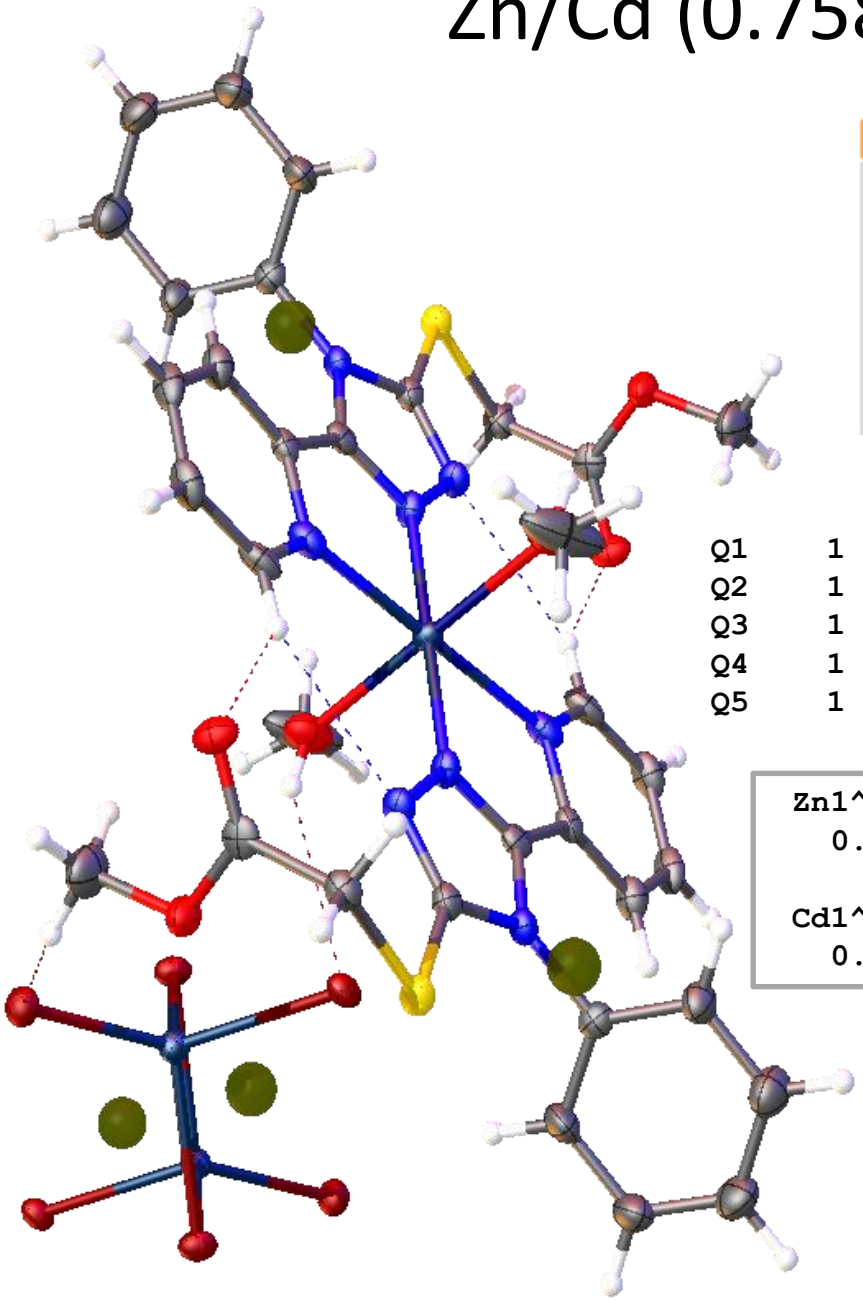
```
PLAT043_ALERT_1_B Calculated and Reported Mol. Weight Differ by ..      112.42 Check
PLAT051_ALERT_1_B Mu(calc) and Mu(CIF) Ratio Differs from 1.0 by .        6.23 %
```

Alert level C

```
PLAT041_ALERT_1_C Calc. and Reported SumFormula    Strings  Differ      Please Check
PLAT052_ALERT_1_C Info on Absorption Correction Method   Not Given      Please Do !
PLAT068_ALERT_1_C Reported F000 Differs from Calcd (or Missing)...      Please Check
PLAT094_ALERT_2_C Ratio of Maximum / Minimum Residual Density ....        2.13 Report
PLAT220_ALERT_2_C Non-Solvent  Resd 1  C   Ueq(max)/Ueq(min) Range        3.8 Ratio
PLAT242_ALERT_2_C Low    'MainMol' Ueq as Compared to Neighbors of        Zn1 Check
PLAT431_ALERT_2_C Short Inter HL..A Contact  Br2       ..S1        .      3.52 Ang.
                                      3/2-x,-1/2+y,1/2-z  =      2_645 Check
PLAT480_ALERT_4_C Long H...A H-Bond Reported H1B       ..BR3       .      3.06 Ang.
PLAT480_ALERT_4_C Long H...A H-Bond Reported H3A       ..BR3       .      3.11 Ang.
PLAT480_ALERT_4_C Long H...A H-Bond Reported H3C       ..BR1       .      3.02 Ang.
PLAT480_ALERT_4_C Long H...A H-Bond Reported H12       ..BR2       .      2.98 Ang.
PLAT911_ALERT_3_C Missing FCF Refl Between Thmin & STh/L=    0.600         16 Report
PLAT971_ALERT_2_C Check Calcd Resid. Dens.  0.37A   From Zn1              2.17 eA-3
PLAT978_ALERT_2_C Number C-C Bonds with Positive Residual Density.          0 Info
```

```
PLAT232_ALERT_2_G Hirshfeld Test Diff (M-X)  Zn1      --O10       .      10.0 s.u.
PLAT232_ALERT_2_G Hirshfeld Test Diff (M-X)  Zn1      --N11       .      12.0 s.u.
PLAT232_ALERT_2_G Hirshfeld Test Diff (M-X)  Zn1      --N12       .       9.0 s.u.
```

Zn/Cd (0.758/0.242) model



Refinement Indicators

R1(Fo > 4sig(Fo))	0.0391	R1(all data)	0.0732
wR2	0.0856	GooF	1.0140
GooF(restr)	1.0140	Highest peak	0.8500
Deepest hole	-0.9400	Params	269
Refs(total)	39302	Refs(uniq)	38522
Refs(Fo > 4sig(Fo))	4673	R(int)	0.0787
R(sigma)	0.0778	F000	1432.7
ρ/g*mm;$^{-3}$	2.090	μ/mm;$^{-1}$	6.55

Q1	1	0.5169	-0.0361	0.0456	1.00000	0.05	-0.94
Q2	1	0.5305	0.0414	0.4131	1.00000	0.05	-0.88
Q3	1	0.4392	0.0380	0.4103	1.00000	0.05	-0.87
Q4	1	0.4992	0.1224	0.4547	1.00000	0.05	-0.86
Q5	1	0.8585	0.1383	0.1189	1.00000	0.05	0.85

Zn1^a	0.50000	0.00000	0.00000	0.37891
0.00000	0.00000	0.00000	0.00000	0.00000
Cd1^b	0.50000	0.00000	0.00000	0.12112
0.00000	0.00000	0.00000	0.00000	0.00079

Zn/Cd model – CheckCIF

```
Bond precision:   C-C = 0.0059 A          Wavelength=0.71073
```

Note how the bond precision improves when we get the strong scatters right.

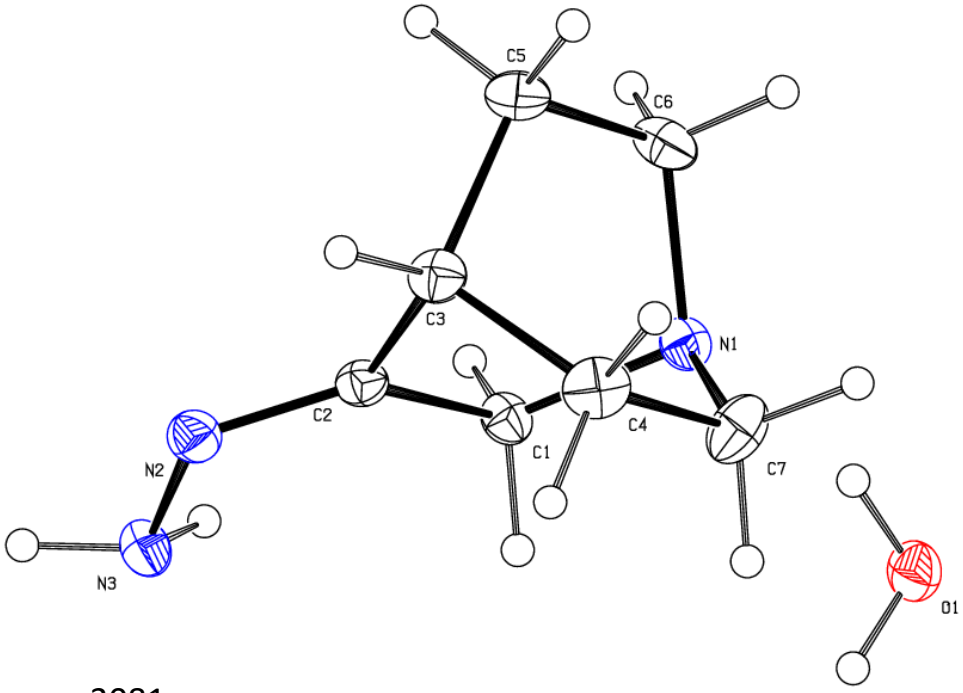
```
PLAT171_ALERT_4_G The CIF-Embedded .res File Contains EADP Records          1 Report
PLAT232_ALERT_2_G Hirshfeld Test Diff (M-X)  Cd1      --O10       .        5.3 s.u.
PLAT232_ALERT_2_G Hirshfeld Test Diff (M-X)  Cd1      --N11       .        7.7 s.u.
PLAT232_ALERT_2_G Hirshfeld Test Diff (M-X)  Zn1      --O10       .        5.3 s.u.
PLAT232_ALERT_2_G Hirshfeld Test Diff (M-X)  Zn1      --N11       .        7.7 s.u.
PLAT300_ALERT_4_G Atom Site Occupancy of Zn1          Constrained at     0.7578 Check
PLAT301_ALERT_3_G Main Residue  Disorder ..............(Resd  1  )          4% Note
```

One of the metal atom sites is a composite of Zn and Cd. Its displacement parameters and the positions of the atoms in the coordination shell will be “apparent” and can fail to adhere to the Hirshfeld test.

You may have to explore your results to understand the origin of an alert.

Example: A Self-Consistency Problem

L. Qiao, X.-G. Chen, J.-X. Gao and Y. Ai (2019). *Acta Cryst.* C**75**, 728-733.
Three new quinuclidine-based structures: second harmonic generation response for 1,2-bis(1-azoniabicyclo[2.2.2]octan-3-ylidene)hydrazine dichloride
Compound 1: $C_7H_{13}N_3 \cdot H_2O$.
(1-Azabicyclo[2.2.2]oct-3-ylidene)hydrazine monohydrate ($P2_1/c$)



qs3081

When a CIF reports geometrical parameters (bond distances, angles, etc., which all CIF invariably have), CheckCIF recalculates these results using the available information – unit cell, symmetry, atomic coordinates – and compares its calculated values to the values reported in the CIF.
If the results do not agree, an alert is raised.

You may have to explore your results to understand the origin of an alert.

Datablock: P21C

Example: A Self-Consistency Problem

```
Bond precision:    C-C = 0.0018 A   Wavelength=0.71073
Cell: a=11.2687(6)  b=8.3690(5)  c=8.9974(5)
      alpha=90  beta=95.724(5)  gamma=90
Temperature: ?
```

	Calculated	Reported
Volume	844.29(8)	844.29(8)
Space group	P 21/c	P 21/c
Hall group	: -P 2ybc	-P 2ybc
Moiety formula	C7 H13 N3, H2 O	C7 H13 N3, H2 O
Sum formula	C7 H15 N3 O	C7 H15 N3 O
Mr	157.22	157.22
Dx,g cm-3	1.237	1.237
Z	4	4
Mu (mm-1)	0.086	0.086
F000	344.0	344.0
F000'	344.12	
h,k,lmax	16,12,12	16,12,12
Nref	2616	2616
Tmin,Tmax	0.974,0.983	0.974,0.983
Tmin'	0.968	

```
Correction method= # Reported   T Limits: Tmin=0.974             Tmax=0.983  AbsCorr =
Data completeness= 1.000
Theta(max)= 30.705
R(reflections)= 0.0394(  1640) wR2(reflections)= 0.0971(  2071)
S = 1.045 Npar= 116
```

Nothing unusual in the global parameters.
But CheckCIF finds that the geometrical parameters calculated by CheckCIF for one of the reported hydrogen bonds do not agree with the geometrical parameters reported in the CIF.

This gives A-level alerts!

Alert level A

```
PLAT706_ALERT_1_A H...A   Calc  13.726(18), Rep    2.042(2), Dev..     649.11 Sigma
                H2       -N3              1.555   2.555 ........     #   26 Check
PLAT707_ALERT_1_A D...A   Calc 13.7449(17), Rep    2.915(2), Dev..    6370.53 Sigma
                O1       -N3              1.555   2.555 ........     #   26 Check
PLAT708_ALERT_1_A D-H..A  Calc    89.4(11), Rep   176.05(2), Dev..      78.77 Sigma
                O1      -H2      -N3          1.555  1.555  2.555     #   47 Check
```

You may have to explore your results to understand the origin of an alert.

Example: A Self-Consistency Problem

```
Alert level A
PLAT706_ALERT_1_A H...A   Calc  13.726(18), Rep    2.042(2), Dev..     649.11 Sigma
                H2       -N3              1.555   2.555 ........     #   26 Check
PLAT707_ALERT_1_A D...A   Calc 13.7449(17), Rep    2.915(2), Dev..    6370.53 Sigma
                O1       -N3              1.555   2.555 ........     #   26 Check
PLAT708_ALERT_1_A D-H..A  Calc    89.4(11), Rep   176.05(2), Dev..      78.77 Sigma
                O1      -H2      -N3         1.555  1.555  2.555     #   47 Check
```

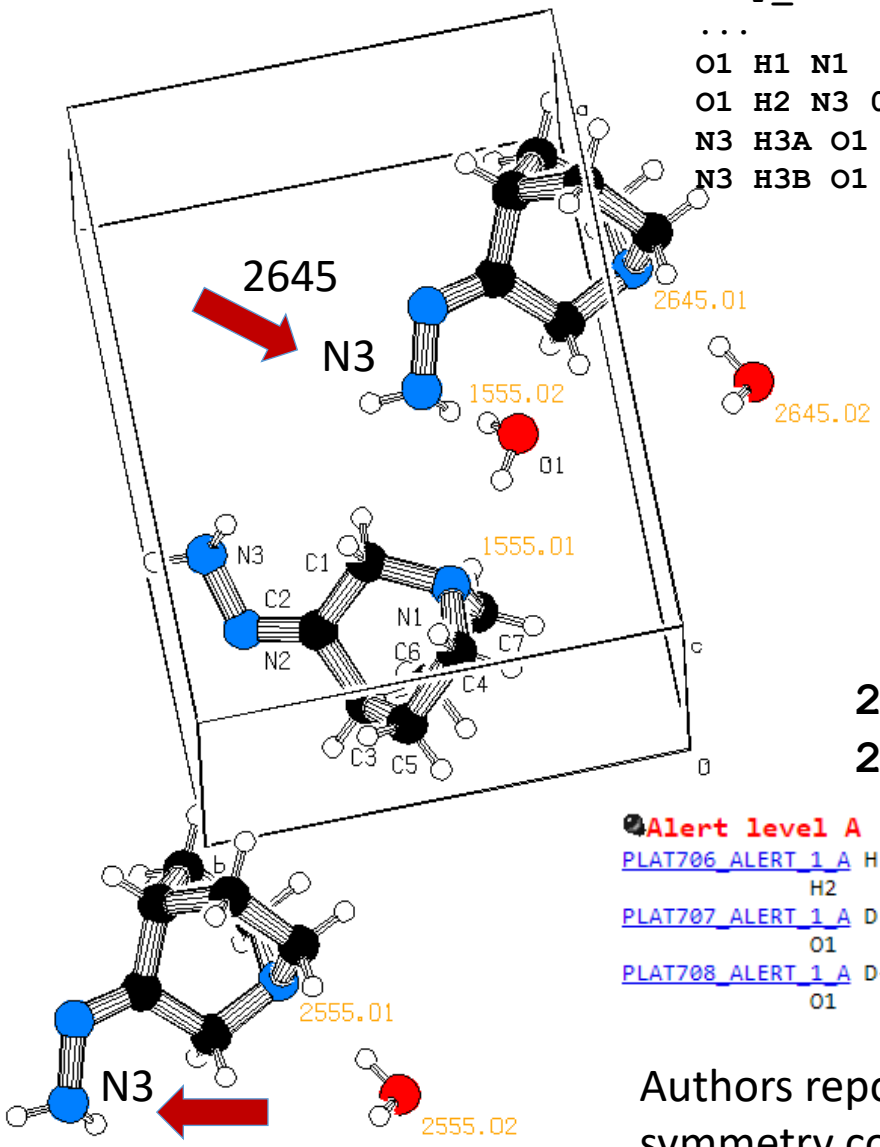
In order to identify the source of this inconsistency, it is necessary to consider the various factors that enter into the calculation of hydrogen-bond geometry. These are the unit cell parameters, the atomic coordinates, and the symmetry operations.

We will look first at the symmetry operation involved in this calculation. From the CIF:

```
loop_
_geom_hbond_atom_site_label_D
_geom_hbond_atom_site_label_H
_geom_hbond_atom_site_label_A
_geom_hbond_distance_DH
_geom_hbond_distance_HA
_geom_hbond_distance_DA
_geom_hbond_angle_DHA
_geom_hbond_site_symmetry_A
O1 H1 N1  0.864(18) 1.994(19) 2.8207(13) 159.9(16)  .
O1 H2 N3 0.874(2) 2.042(2) 2.915(2) 176.05(2) 2_555
N3 H3A O1  0.908(17) 2.186(17) 3.0517(15) 159.3(14) 3_666
N3 H3B O1  0.898(17) 2.212(17) 3.0529(15) 155.6(13) 1_565
```

```
loop_
_space_group_symop_operation_xyz
'x, y, z'
'-x, y+1/2, -z+1/2'
'-x, -y, -z'
'x, -y-1/2, z-1/2'
```

You may have to explore your results to understand the origin of an alert.




```
loop_
...
O1 H1 N1   0.864(18) 1.994(19) 2.8207(13) 159.9(16)  .
O1 H2 N3  0.874(2) 2.042(2) 2.915(2) 176.05(2) 2_555
N3 H3A O1   0.908(17) 2.186(17) 3.0517(15) 159.3(14) 3_666
N3 H3B O1   0.898(17) 2.212(17) 3.0529(15) 155.6(13) 1_565
```

```
loop_
_space_group_symop_operation_xyz
'x, y, z'
'-x, y+1/2, -z+1/2'
'-x, -y, -z'
'x, -y-1/2, z-1/2'
```

2555: -x, y+1/2, -z+1/2

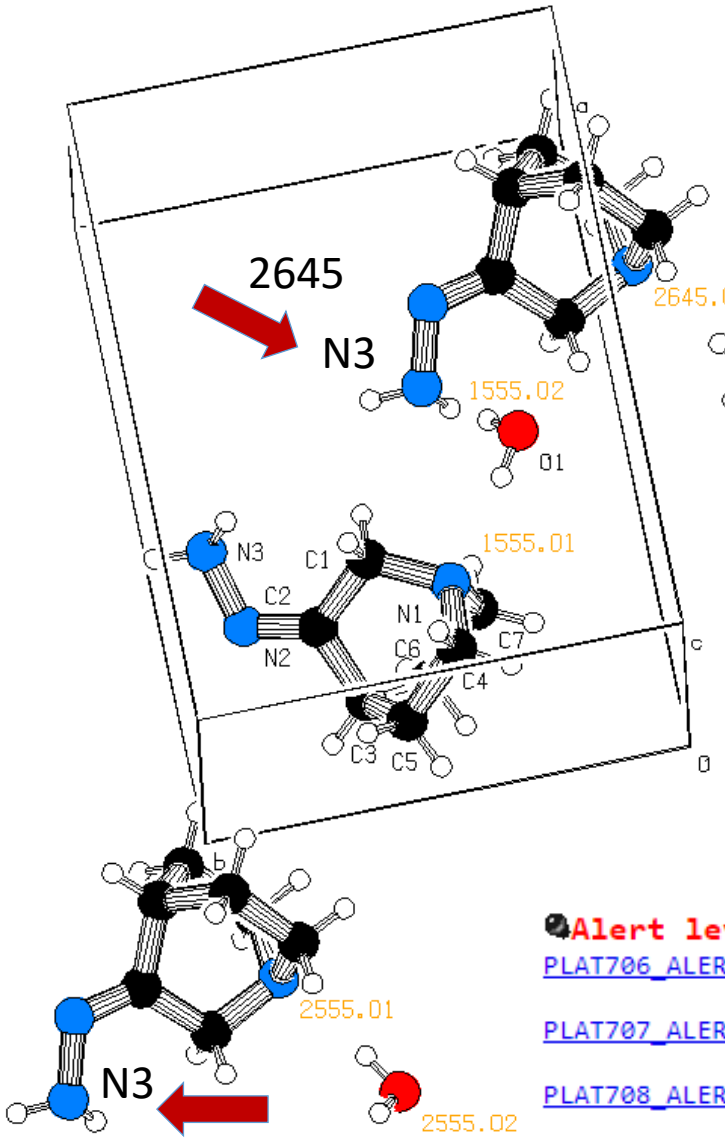
2645: 1-x, y-1/2, -z+1/2

Alert level A

PLAT706_ALERT_1_A H...A Calc 13.726(18), Rep 2.042(2), Dev.. 649.11 Sigma
H2 -N3 1.555 2.555 ..... # 26 Check
PLAT707_ALERT_1_A D...A Calc 13.7449(17), Rep 2.915(2), Dev.. 6370.53 Sigma
O1 -N3 1.555 2.555 ..... # 26 Check
PLAT708_ALERT_1_A D-H..A Calc 89.4(11), Rep 176.05(2), Dev.. 78.77 Sigma
O1 -H2 -N3 1.555 1.555 2.555 # 47 Check

Authors report the correct geometry with the incorrect symmetry code for the Acceptor. How did this happen?

You may have to explore your results to understand the origin of an alert.



ShelxL Instructions:
EQIV $n symmetry operation
Defines symmetry operation $n for referencing symmetry equivalent atoms on any instruction which allows atom names, by appending '_$n' (where n is an integer between 1 and 511 inclusive) to the atom name. Such a symmetry operation must be defined before it is used;

```
ShelxL .LST file:
Specified hydrogen bonds (with esds except fixed and riding H)
  D-H          H...A         D...A         <(DHA)
0.864(18)    1.994(19)    2.8207(13)    159.9(16)    O1-H1...N1
 ** No suitable H-bond found for O1...N2_$1 = 3.4153(15) A **
 ** No suitable H-bond found for O1...N3_$1 = 2.9148(15) A **
```

2555: -x, y+1/2, -z+1/2
2645: 1-x, y-1/2, -z+1/2

Alert level A

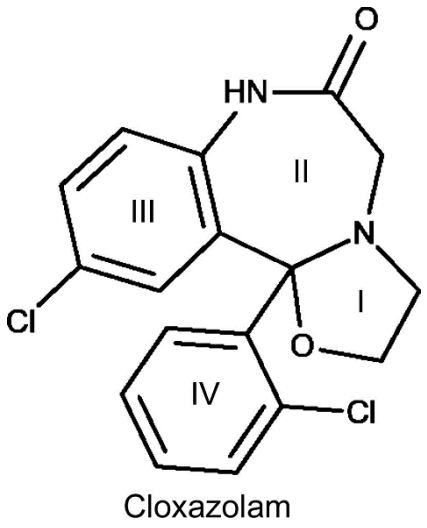
PLAT706_ALERT_1_A H...A Calc 13.726(18), Rep 2.042(2), Dev.. 649.11 Sigma
H2 -N3 1.555 2.555 ..... # 26 Check
PLAT707_ALERT_1_A D...A Calc 13.7449(17), Rep 2.915(2), Dev.. 6370.53 Sigma
O1 -N3 1.555 2.555 ..... # 26 Check
PLAT708_ALERT_1_A D-H..A Calc 89.4(11), Rep 176.05(2), Dev.. 78.77 Sigma
O1 -H2 -N3 1.555 1.555 2.555 # 47 Check

When to explain your model rather than to change it

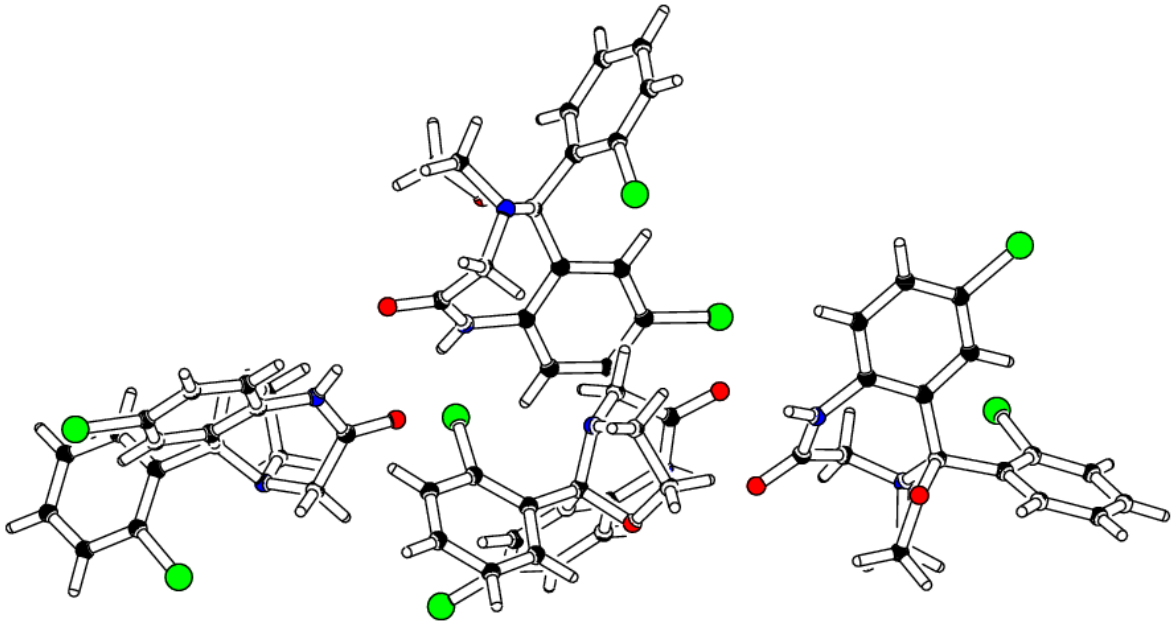
SK3730: María Soledad Garraza, María Emilia Gimenez, Daniel Roberto Vega and Ricardo Baggio*

Crystal structure and pseudosymmetry analysis of the triclinic prodrug cloxazolam (Z' = 4)

Acta Cryst. (2019) **C75**, 851-858. doi: 10.1107/S2053229619008404



Cloxazolam



There are four molecules in the unit cell, with pronounced pseudosymmetry. The authors found it convenient to use a double cell with the unconventional space group B(-1).

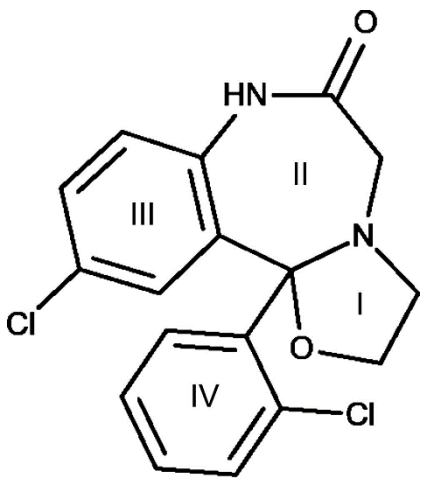
When to explain your model rather than to change it

SK3730: María Soledad Garraza, María Emilia Gimenez, Daniel Roberto Vega and Ricardo Baggio*
Crystal structure and pseudosymmetry analysis of the triclinic prodrug cloxazolam (Z' = 4)
Acta Cryst. (2019) **C75**,

"…when the four-membered group in the asymmetric unit was analyzed for eventual hidden relationships, a number of pseudosymmetry operations were readily apparent."

"In order to make this symmetry analysis more easily comprehensible, the description of the crystal structure has been made in the centred nonconventional B(-1) spacegroup setting[1]."

[1] The original reduced triclinic unit cell, as determined in the data-collection procedure, was a' = 12.6268 (6), b' = 15.0541 (6), c' = 17.0054 (7) Å , α' = 81.837 (2), β' = 80.311 (2), γ' = 74.146 (2)^o, V' = 3049.4 (2) Å^3, space group P-1. With the transformation matrix M = (1 -1 0, 0 0 1, 1 1 0), the centred nonconventional unit cell we are working with is obtained: a = 16.7989 (6), b = 17.0054 (7), c = 22.1341 (7) Å , α = 78.897 (2), β = 100.411 (2), γ = 90.042 (3)^o, V = 2V' = 6098.8 (4) Å^3, space group B-1. In this unit cell, the triad (a,b,c*) defines an almost perfect orthogonal reference frame, suitable for describing the pseudosymmetry of the current structure.



Cloxazolam

When to explain your model rather than to change it

SK3730: María Soledad Garraza, María Emilia Gimenez, Daniel Roberto Vega and Ricardo Baggio*

Crystal structure and pseudosymmetry analysis of the triclinic prodrug cloxazolam (Z' = 4) *Acta Cryst.* (2019) **C75**,

Alert level A

SYMMG01_ALERT_1_A Unrecognised _symmetry_space_group_name_H-M

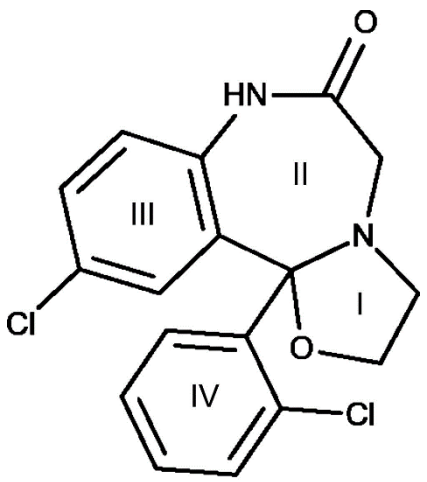
```
From the CIF: _space_group_IT_number       1
From the CIF: _symmetry_space_group_name_H-M      B -1
Int. Tables space group number for B -1 is   0
```

Author Response: As explained in the text, in order to make pseudo-symmetry analysis more easily comprehensible, the crystallographic description has been performed in a redundant, non-conventional space group, the centred triclinic B-1, with two nodes per cell, instead of the conventional P-1, with one single node.

SYMMG02_ALERT_1_A Supplied _symmetry_space_group_name_H-M not recognised

```
From the CIF: _symmetry_equiv_pos_as_xyz
                                  x, y, z
                                  x+1/2, y, z+1/2
                                  -x, -y, -z
                                  -x+1/2, -y, -z+1/2
These symops generate the Hall space group symbol   -b_1
 which is equivalent to the H-M space group symbol
```

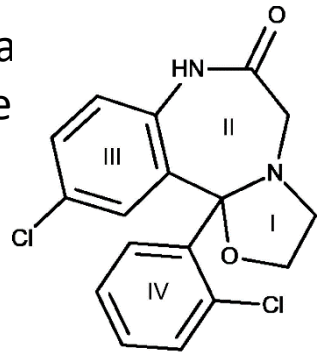
Author Response: see above



Cloxazolam

When to explain your model rather than to change it

SK3730: María Soledad Garraza, María Emilia Gimenez, Daniel Roberto Vega and Ricardo Baggio.* Crystal structure and pseudosymmetry analysis of the triclinic prodrug cloxazolam (Z' = 4). *Acta Cryst.* (2019) **C75**,



Cloxazolam

Alert level C

PLAT048_ALERT_1_C MoietyFormula Not Given (or Incomplete) ..... Please Check
PLAT094_ALERT_2_C Ratio of Maximum / Minimum Residual Density .... 2.77 Report

Author Response: Both the Maximum and Minimum Residual Density are well within expected values for a medium quality organic structure,

PLAT155_ALERT_4_C The Triclinic Unitcell is NOT Reduced ..... Please Do !

Author Response: see above

PLAT340_ALERT_3_C Low Bond Precision on C-C Bonds ..... 0.0048 Ang.
PLAT480_ALERT_4_C Long H...A H-Bond Reported H10B ..CL1D . 2.99 Ang.

Author Response: Even if weak, these interactions are obviously real, as assessed by the supramolecular discussion included

PLAT480_ALERT_4_C Long H...A H-Bond Reported H9D ..CL1A . 2.97 Ang.

Author Response: Even if weak, these interactions are obviously real, as assessed by the supramolecular discussion included

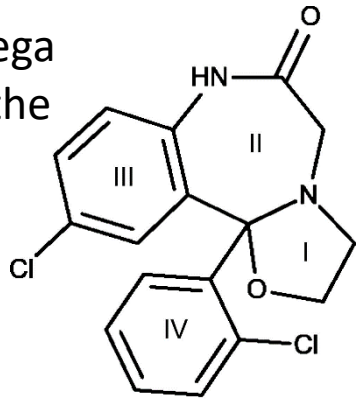
PLAT480_ALERT_4_C Long H...A H-Bond Reported H17C ..CL2D . 2.95 Ang.

Author Response: Even if weak, these interactions are obviously real, as assessed by the supramolecular discussion included

PLAT906_ALERT_3_C Large K Value in the Analysis of Variance ..... 4.050 Check
PLAT910_ALERT_3_C Missing # of FCF Reflection(s) Below Theta(Min). 7 Note
PLAT978_ALERT_2_C Number C-C Bonds with Positive Residual Density. 0 Info

When to explain your model rather than to change it

SK3730: María Soledad Garraza, María Emilia Gimenez, Daniel Roberto Vega and Ricardo Baggio.* Crystal structure and pseudosymmetry analysis of the triclinic prodrug cloxazolam (Z' = 4). *Acta Cryst.* (2019) **C75**,



Cloxazolam

Alert level G

PLAT002_ALERT_2_G	Number of Distance or Angle Restraints on AtSite	8	Note
PLAT128_ALERT_4_G	Alternate Setting for Input Space Group B-1	P-1	Note
PLAT172_ALERT_4_G	The CIF-Embedded .res File Contains DFIX Records	1	Report
PLAT398_ALERT_2_G	Deviating C-O-C Angle From 120 for O1A	108.9	Degree
PLAT398_ALERT_2_G	Deviating C-O-C Angle From 120 for O1B	108.5	Degree
PLAT398_ALERT_2_G	Deviating C-O-C Angle From 120 for O1C	108.0	Degree
PLAT398_ALERT_2_G	Deviating C-O-C Angle From 120 for O1D	108.4	Degree
PLAT432_ALERT_2_G	Short Inter X...Y Contact Cl2D ..C16B	3.21	Ang.
	-x,2-y,1-z =	3_576	Check
PLAT790_ALERT_4_G	Centre of Gravity not Within Unit Cell: Resd. #	4	Note
	C17 H14 Cl2 N2 O2		
PLAT793_ALERT_4_G	Model has Chirality at C1A (Centro SPGR)	S	Verify
PLAT793_ALERT_4_G	Model has Chirality at C1B (Centro SPGR)	S	Verify
PLAT793_ALERT_4_G	Model has Chirality at C1C (Centro SPGR)	S	Verify
PLAT793_ALERT_4_G	Model has Chirality at C1D (Centro SPGR)	S	Verify
PLAT860_ALERT_3_G	Number of Least-Squares Restraints	4	Note
PLAT912_ALERT_4_G	Missing # of FCF Reflections Above STh/L= 0.600	25	Note

Acta Cryst., Section C: Structural Chemistry (2014), 70(9), 834-836.

DOI:10.1107/S2053229614017549

FA3343 September, 2014

scientific comment

Acta Crystallographica Section C
Structural Chemistry
ISSN 2053-2296

Some more space-group corrections

Lawrence M. Henling and Richard E. Marsh*

Beckman Institute, California Institute of Technology, Caltech 139-74, Pasadena, CA 91125, USA
Correspondence e-mail: rmarsh@caltech.edu

Received 11 May 2014
Accepted 30 July 2014

A survey of approximately 100 000 entries in recent releases of the Cambridge Structural Database (CSD) has uncovered 156 crystal structures that were apparently described in inappropriate space groups. We have revised these space groups and prepared CIFs containing the new coordinates and brief comments describing the revisions.

Keywords: space-group corrections; Cambridge Structural Database (CSD) survey; database survey.

1. Introduction

It is the purpose of this paper to report on the reliability of small-molecule crystal-structure results in recent years, when computers have essentially replaced human beings in the entire process of determining a structure. A rough estimate of the incidence of inappropriate assignments to space group *P*1 (the most common miscreant) suggests that they now occur slightly less than 2% of the time – far less than the 10% frequency that one of us observed in a 2005 survey (Marsh, 2005). This is indeed good news.

We greatly appreciate the help of Michael Takase, who carried out some of the calculations and participated in many of our discussions about the various compounds.

References

Spek, A. L. (2009). *Acta Cryst.* **D65**, 148-155. Structural validation in chemical crystallography. doi: 10.1107/S090744490804362X